

## SEQUENCE LISTING

<110> Ganymed Pharmaceuticals AG  
 TURECI, Ozlem  
 SAHIN, Ugur  
 HELFTENBEIN, Gerd  
 SCHLUTER, Volker

<120> Identification of Tumour-Associated Cell Surface Antigens for Diagnosis and Therapy

<130> VOS-203

<140> US10/573,229

<141> 2006-03-24

<150> PCT/EP2004/010697

<151> 2004-09-23

<150> DE 103 44 799.7

<151> 2003-09-26

<160> 312

<170> PatentIn Version 3.1

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Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile  
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Ser Val Met Asn Gly Ile Cys Leu Leu Leu Ala Ala Val Thr Val Lys
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Leu Tyr Ser Ser Phe Asp Phe Asn Cys Pro Cys Leu Val His Tyr Asn
35             40             45

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Ala Leu Tyr Gly Leu Gly Leu Leu Leu Thr Pro Pro Leu Ala Leu Phe
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Glu Leu Val Arg Asp Ser Pro Ala Arg Lys Ala Val Ser Arg Tyr Leu  
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Val Phe Leu Gln Arg Arg Tyr Trp Ser Asn Tyr Val Asp Leu Glu Gln  
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Trp Tyr Ser Ser Lys Pro Pro Leu Asp Leu Ala Ala Ser Pro Gly Leu  
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Pro Gly Ala Arg Thr Ala Glu Gly Pro Ile Met Val Leu Ala Gly Pro  
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Leu Ala Val Ser Leu Leu Leu Pro Ser Leu Thr Leu Leu Val Ser His  
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Leu Ser Ser Ser Gln Asp Val Ser Ser Glu Pro Ser Ser Glu Gln Gln  
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Leu Cys Ala Leu Ser Lys His Pro Thr Val Ala Phe Glu Asp Leu Gln  
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Pro Trp Val Ser Asn Phe Thr Tyr Pro Gly Ala Arg Asp Phe Ser Gln  
 115 120 125

Leu Ala Leu Asp Pro Ser Gly Asn Gln Leu Ile Val Gly Ala Arg Asn  
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Tyr Leu Phe Arg Leu Ser Leu Ala Asn Val Ser Leu Leu Gln Ala Thr  
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Glu Trp Ala Ser Ser Glu Asp Thr Arg Arg Ser Cys Gln Ser Lys Gly  
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Lys Thr Glu Glu Glu Cys Gln Asn Tyr Val Arg Val Leu Ile Val Ala  
 180 185 190

Gly Arg Lys Val Phe Met Cys Gly Thr Asn Ala Phe Ser Pro Met Cys  
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Thr Ser Arg Gln Val Gly Asn Leu Ser Arg Thr Ile Glu Lys Ile Asn  
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Gly Val Ala Arg Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val  
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Ile Ser Ser Gln Gly Glu Leu Tyr Ala Ala Thr Val Ile Asp Phe Ser  
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Gly Arg Asp Pro Ala Ile Tyr Arg Ser Leu Gly Ser Gly Pro Pro Leu  
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Arg Thr Ala Gln Tyr Asn Ser Lys Trp Leu Asn Glu Pro Asn Phe Val  
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Ala Ala Tyr Asp Ile Gly Leu Phe Ala Tyr Phe Phe Leu Arg Glu Asn  
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Ala Val Glu His Asp Cys Gly Arg Thr Val Tyr Ser Arg Val Ala Arg  
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Val Cys Lys Asn Asp Val Gly Gly Arg Phe Leu Leu Glu Asp Thr Trp  
 325 330 335

Thr Thr Phe Met Lys Ala Arg Leu Asn Cys Ser Arg Pro Gly Glu Val  
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Pro Phe Tyr Tyr Asn Glu Leu Gln Ser Ala Phe His Leu Pro Glu Gln  
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Asp Leu Ile Tyr Gly Val Phe Thr Thr Asn Val Asn Ser Ile Ala Ala  
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Ser Ala Val Cys Ala Phe Asn Leu Ser Ala Ile Ser Gln Ala Phe Asn  
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Gly Pro Phe Arg Tyr Gln Glu Asn Pro Arg Ala Ala Trp Leu Pro Ile  
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Ala Asn Pro Ile Pro Asn Phe Gln Cys Gly Thr Leu Pro Glu Thr Gly  
 420 425 430

Pro Asn Glu Asn Leu Thr Glu Arg Ser Leu Gln Asp Ala Gln Arg Leu  
 435 440 445

Phe Leu Met Ser Glu Ala Val Gln Pro Val Thr Pro Glu Pro Cys Val  
 450 455 460

Thr Gln Asp Ser Val Arg Phe Ser His Leu Val Val Asp Leu Val Gln  
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Ala Lys Asp Thr Leu Tyr His Val Leu Tyr Ile Gly Thr Glu Ser Gly  
 485 490 495

Thr Ile Leu Lys Ala Leu Ser Thr Ala Ser Arg Ser Leu His Gly Cys  
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Tyr Leu Glu Glu Leu His Val Leu Pro Pro Gly Arg Arg Glu Pro Leu  
 515 520 525

Arg Ser Leu Arg Ile Leu His Ser Ala Arg Ala Leu Phe Val Gly Leu  
 530 535 540

Arg Asp Gly Val Leu Arg Val Pro Leu Glu Arg Cys Ala Ala Tyr Arg  
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Ser Gln Gly Ala Cys Leu Gly Ala Arg Asp Pro Tyr Cys Gly Trp Asp  
 565 570 575

Gly Lys Gln Gln Arg Cys Ser Thr Leu Glu Asp Ser Ser Asn Met Ser  
 580 585 590

Leu Trp Thr Gln Asn Ile Thr Ala Cys Pro Val Arg Asn Val Thr Arg  
 595 600 605

Asp Gly Gly Phe Gly Pro Trp Ser Pro Trp Gln Pro Cys Glu His Leu  
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Asp Gly Asp Asn Ser Gly Ser Cys Leu Cys Arg Ala Arg Ser Cys Asp  
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Ser Pro Arg Pro Arg Cys Gly Gly Leu Asp Cys Leu Gly Pro Ala Ile  
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His Ile Ala Asn Cys Ser Arg Asn Gly Ala Trp Thr Pro Trp Ser Ser  
 660 665 670

Trp Ala Leu Cys Ser Thr Ser Cys Gly Ile Gly Phe Gln Val Arg Gln  
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Arg Ser Cys Ser Asn Pro Ala Pro Arg His Gly Gly Arg Ile Cys Val  
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Gly Lys Ser Arg Glu Glu Arg Phe Cys Asn Glu Asn Thr Pro Cys Pro  
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Val Pro Ile Phe Trp Ala Ser Trp Gly Ser Trp Ser Lys Cys Ser Ser  
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Asn Cys Gly Gly Gly Met Gln Ser Arg Arg Arg Ala Cys Glu Asn Gly  
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Asn Ser Cys Leu Gly Cys Gly Val Glu Phe Lys Thr Cys Asn Pro Glu  
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Gly Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr Pro Trp Leu Pro  
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Pro His Thr Val Ser Gly Gly Trp Ala Ala Trp Gly Pro Trp Ser Ser  
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Cys Ser Arg Asp Cys Glu Leu Gly Phe Arg Val Arg Lys Arg Thr Cys  
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Leu Pro Gly Ser Ser Ala Cys Ala Gly Asn Ser Ser Gln Ser Arg Pro  
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Cys Pro Tyr Ser Glu Ile Pro Val Ile Leu Pro Ala Ser Ser Met  
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Glu Glu Ala Thr Asp Cys Ala Gly Phe Asn Leu Ile His Leu Val  
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Ala Thr Gly Ile Ser Cys Phe Leu Gly Ser Gly Leu Leu Thr Leu  
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Ala Val Tyr Leu Ser Cys Gln His Cys Gln Arg Gln Ser Gln Glu  
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Ser Thr Leu Val His Pro Ala Thr Pro Asn His Leu His Tyr Lys  
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Lys Thr Leu Asn Lys Asn Asn Leu Ile Pro Asp Asp Arg Ala Asn  
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Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
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Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
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Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65           70           75           80

```

```

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85           90           95

```

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn  
 100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp  
 115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala  
 130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro  
 145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe  
 165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala  
 180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu  
 195 200 205

Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala  
 210 215 220

Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln  
 225 230 235 240

Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His  
 245 250 255

Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile  
 260 265 270

Leu

<210> 27  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 27  
 ggagtagtca ctcagtagca gc

<210> 28  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 28  
 gaactcatca aagcagacg 19

<210> 29  
 <211> 1528  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 ggaaggcaca ggcctgagaa gtctgcggct gagctgggag caaatcccc acccctacc 60  
 tgggggacag ggcaagtgag acctggtgag ggtggctcag caggaaggga aggagaggtg 120  
 tctgtgcgtc ctgcaccac atctttctct gtccctcct tgccctgtct ggaggctgct 180  
 agactcctat cttctgaatt ctatagtgcc tgggtctcag cgcagtgccg atggtggccc 240  
 gtccttgtgg ttctctctta cctggggaaa taagggtgcag cggccatggc tacagcaaga 300  
 cccccctgga tgtgggtgct ctgtgctctg atcacagcct tgcttctggg ggtcacagag 360  
 catgttctcg ccaacaatga tgtttctgt gaccaccct ctaacaccgt gccctctggg 420  
 agcaaccagg acctgggagc tggggccggg gaagacgccc ggtcggatga cagcagcagc 480  
 cgcacatca atggatccga ctgcgatatg cacaccagc cgtggcaggc cgcgctgttg 540  
 ctaaggccca accagctcta ctgcggggcg gtgttggtgc atccacagtg gctgctcacg 600  
 gccgccact gcaggaagaa agttttcaga gtccgtctcg gccactact cctgtcacca 660  
 gtttatgaat ctgggcagca gatgttccag ggggtcaa atccatcccc cctgggtac 720  
 tcccaccctg gccactctaa cgacctcatg ctcatcaaac tgaacagaag aattcgtccc 780  
 actaaagatg tcagacccat caacgtctcc tctcattgtc cctctgctgg gacaaagtgc 840  
 ttggtgtctg gctgggggac aaccaagagc cccaagtgc acttccctaa ggtcctccag 900  
 tgcttgaata tcagcgtgct aagtcagaaa aggtgcgagg atgcttacc gagacagata 960  
 gatgacacca tgttctgcgc cggtgacaaa gcaggtagag actcctgcca gggtgattct 1020  
 ggggggcctg tggctctcaa tggctccctg cagggactcg tgcctgggg agattaccct 1080  
 tgtgcccggc ccaacagacc ggggtgtctac acgaacctct gcaagttcac caagtggatc 1140  
 caggaaacca tccaggccaa ctctgagtc atccaggac tcagcacacc ggcatcccca 1200

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cctgctgcag ggacagccct gacactcctt tcagaccctc attccttccc agagatgttg 1260
agaatgttca tctctccagc ccctgacccc atgtctcctg gactcagggt ctgcttcccc 1320
cacattgggc tgaccgtgtc tctctagttg aaccctggga acaatttcca aaactgtcca 1380
gggcgggggt tgcgtctcaa tctccctggg gcactttcat cctcaagctc agggcccatc 1440
ccttctctgc agctctgacc caaatttagt cccagaaata aactgagaag tggaaaaaaaa 1500
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1528

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<210> 30
<211> 293
<212> PRT
<213> Homo sapiens

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<400> 30

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Met Ala Thr Ala Arg Pro Pro Trp Met Trp Val Leu Cys Ala Leu Ile
1          5          10          15

```

```

Thr Ala Leu Leu Leu Gly Val Thr Glu His Val Leu Ala Asn Asn Asp
20          25          30

```

```

Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly Ser Asn Gln
35          40          45

```

```

Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser Asp Asp Ser Ser
50          55          60

```

```

Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met His Thr Gln Pro Trp
65          70          75          80

```

```

Gln Ala Ala Leu Leu Leu Arg Pro Asn Gln Leu Tyr Cys Gly Ala Val
85          90          95

```

```

Leu Val His Pro Gln Trp Leu Leu Thr Ala Ala His Cys Arg Lys Lys
100         105         110

```

```

Val Phe Arg Val Arg Leu Gly His Tyr Ser Leu Ser Pro Val Tyr Glu
115         120         125

```

```

Ser Gly Gln Gln Met Phe Gln Gly Val Lys Ser Ile Pro His Pro Gly
130         135         140

```

```

Tyr Ser His Pro Gly His Ser Asn Asp Leu Met Leu Ile Lys Leu Asn
145         150         155         160

```

Arg Arg Ile Arg Pro Thr Lys Asp Val Arg Pro Ile Asn Val Ser Ser  
 165 170 175

His Cys Pro Ser Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr  
 180 185 190

Thr Lys Ser Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn  
 195 200 205

Ile Ser Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln  
 210 215 220

Ile Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser  
 225 230 235 240

Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu Gln  
 245 250 255

Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn Arg Pro  
 260 265 270

Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Lys Trp Ile Gln Glu Thr  
 275 280 285

Ile Gln Ala Asn Ser  
 290

<210> 31  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 31  
 cagaaaaggt gcgaggatg

19

<210> 32  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 32  
 ctgggatgac tcaggagttg g

21

<210> 33  
 <211> 636  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 atgacagaag cagcatcgct tgtccctaag aggccaagga ggctcagagg cagccacaag 60  
 ctgcgagtgc tggcatggcc agtggtcgtg gtggtgaact ttgtttggca gtgcaacggc 120  
 agcattgctc acaccttcct ggagctaagc ttcgcctgcc ctggaggaag gtacgcaggc 180  
 agtcgcccag ccccggttgc agggatggac cgcgaccagc agagggcaga aagtgcctgt 240  
 gtccccatt ctgatcccg gggccccaac ctcccatcgg ctccagtcctc cgcccaatct 300  
 ctgccaggcc cggagctttc ccagaccctt caccacact ccaggctcac tccccgttcc 360  
 tgggcctggg ccccccttgc acgagtccag ggccagccgt cctcgccttc tgcccgcccc 420  
 cgtccttcgt tcttgggagc cggccctctc cgcggaccaa gcggccccga gcaggcgccg 480  
 ccgcccgggg gactccgact cagccccgcg gacctacctc ggccgacagt cggggggttcc 540  
 caagcggccca ctcccggccg gcgccgtccc ctggcggagc cgccgcgctc cctgccgtcc 600  
 gcgcagtcctg gcctcgctcg gggccactcc tcgtag 636

<210> 34  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Thr Glu Ala Ala Ser Leu Val Pro Lys Arg Pro Arg Arg Leu Arg  
 1 5 10 15  
 Gly Ser His Lys Leu Arg Val Leu Ala Trp Pro Val Val Val Val Val  
 20 25 30  
 Asn Phe Val Trp Gln Cys Asn Gly Ser Ile Ala His Thr Phe Leu Glu  
 35 40 45  
 Leu Ser Phe Ala Cys Pro Gly Gly Arg Tyr Ala Gly Ser Arg Pro Ala  
 50 55 60  
 Pro Val Ala Gly Met Asp Arg Asp Gln Gln Arg Ala Glu Ser Ala Cys  
 65 70 75 80  
 Val Pro His Ser Arg Ser Arg Gly Pro Asn Leu Pro Ser Ala Gln Ser  
 85 90 95

Pro Ala Gln Ser Leu Pro Gly Pro Glu Leu Ser Gln Thr Pro His Pro  
 100 105 110

His Ser Arg Leu Thr Pro Arg Ser Trp Ala Trp Ala Pro Leu Ala Arg  
 115 120 125

Val Gln Gly Gln Pro Ser Ser Pro Ser Ala Arg Pro Arg Pro Ser Phe  
 130 135 140

Leu Gly Ala Gly Pro Leu Arg Gly Pro Ser Gly Pro Glu Gln Ala Pro  
 145 150 155 160

Pro Pro Gly Gly Leu Arg Leu Ser Pro Arg Asp Leu Pro Arg Pro Thr  
 165 170 175

Val Gly Gly Ser Gln Ala Ala Thr Pro Gly Arg Arg Arg Pro Leu Ala  
 180 185 190

Glu Pro Pro Arg Ser Leu Pro Ser Ala Gln Ser Gly Leu Ala Arg Gly  
 195 200 205

His Ser Ser  
 210

<210> 35  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 35  
 tgctctcact gtggtcctca g 21

<210> 36  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 36  
 tttgtaaagc tccagcgcta c 21

<210> 37  
 <211> 969  
 <212> DNA  
 <213> Homo sapiens

<400> 37  
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ctcttctctg aagctgccct gcccccttat cgtctttccc aagggcactt cctcacagcc 120  
ctggggggcc tcatggcggt gccattcatc ctggccaagg acctgtgcct gcagcaggac 180  
cccctgacac agagctacct catcagcacc attttctttg ctccagcatc tgcagtctcc 240  
tgcaagctgc ccattcccca gggaggtacg tttgcttttg tggtaatttc tctggccatg 300  
ctctcccttc cctcctggaa ttgccctgag tggacactca gtgccagcca ggtgaacacc 360  
aactttccag aattcactca gaaatggcag aagaggatcc aagaggggtgc tatcatggtc 420  
acttctgtg tccggatgct ggtgggcttc tcaggcctga ctggctttct catgggtttc 480  
atctgctcct tggccgttgc tccaactaac tgcctagtgg cctgccccct cttggattct 540  
gcaggcaata atgccgggat ccagtggggg atttctgcca tgtattgctt cgtgttgct 600  
cttcgcaagg atgagctctg gccatttggg tctccacggc tgcgtttgcc accatcccca 660  
ccccgtgatc ggaggcatgt cccaccccc gtgatcggag gcatgaccct gtttggggtc 720  
atcactgccg tggggatctc caatctgcag tacgtggaca tgaacttgtc caggagcctc 780  
ttcgctttg gcttctccat ctactgtggg ctcaccattc ccaaccgggt gagcaaaaac 840  
cccagatgc tccagacagg gattctccag ccggaccagg ttgttcagat gctgctgacc 900  
atgggcatgt tcatcagtgg atttctgggt tttcttctag acaacaccat ccccgagctc 960  
cttcaataa 969

<210> 38  
<211> 322  
<212> PRT  
<213> Homo sapiens

<400> 38

Met Lys Asp Cys Arg Asn Asn Gly Lys Asp Cys Gln Ser Ala Pro Ala  
1 5 10 15

Thr Arg Arg His Leu Phe Ser Glu Ala Ala Leu Pro Pro Tyr Arg Leu  
20 25 30

Ser Gln Gly His Phe Leu Thr Ala Leu Gly Gly Leu Met Ala Val Pro  
35 40 45

Phe Ile Leu Ala Lys Asp Leu Cys Leu Gln Gln Asp Pro Leu Thr Gln  
50 55 60



Ser Tyr Leu Ile Ser Thr Ile Phe Phe Ala Pro Ala Ser Ala Cys Ser  
 65 70 75 80  
 Cys Lys Leu Pro Ile Pro Gln Gly Gly Thr Phe Ala Phe Val Val Ile  
 85 90 95  
 Ser Leu Ala Met Leu Ser Leu Pro Ser Trp Asn Cys Pro Glu Trp Thr  
 100 105 110  
 Leu Ser Ala Ser Gln Val Asn Thr Asn Phe Pro Glu Phe Thr Gln Lys  
 115 120 125  
 Trp Gln Lys Arg Ile Gln Glu Gly Ala Ile Met Val Thr Ser Cys Val  
 130 135 140  
 Arg Met Leu Val Gly Phe Ser Gly Leu Thr Gly Phe Leu Met Gly Phe  
 145 150 155 160  
 Ile Cys Ser Leu Ala Val Ala Pro Thr Asn Cys Leu Val Ala Leu Pro  
 165 170 175  
 Leu Leu Asp Ser Ala Gly Asn Asn Ala Gly Ile Gln Trp Gly Ile Ser  
 180 185 190  
 Ala Met Tyr Cys Phe Val Leu Arg Leu Arg Lys Asp Glu Leu Trp Pro  
 195 200 205  
 Phe Gly Ser Pro Arg Leu Arg Leu Pro Pro Ser Pro Pro Arg Asp Arg  
 210 215 220  
 Arg His Val Pro Thr Pro Val Ile Gly Gly Met Thr Leu Phe Gly Val  
 225 230 235 240  
 Ile Thr Ala Val Gly Ile Ser Asn Leu Gln Tyr Val Asp Met Asn Leu  
 245 250 255  
 Ser Arg Ser Leu Phe Ala Phe Gly Phe Ser Ile Tyr Cys Gly Leu Thr  
 260 265 270  
 Ile Pro Asn Arg Val Ser Lys Asn Pro Glu Met Leu Gln Thr Gly Ile  
 275 280 285  
 Leu Gln Pro Asp Gln Val Val Gln Met Leu Leu Thr Met Gly Met Phe  
 290 295 300

Ile	Ser	Gly	Phe	Leu	Gly	Phe	Leu	Leu	Asp	Asn	Thr	Ile	Pro	Glu	Leu
305					310					315					320

Leu Gln

<210> 39  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 39  
 atggcggtgc cattcatcct 20

<210> 40  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 40  
 caggagggaa gggagagcat 20

<210> 41  
 <211> 1679  
 <212> DNA  
 <213> Homo sapiens

<400> 41  
 gaggaggcgc gcgtcgccgc cccgcgtccc gcctgcggcc cgcgcccccg gcgtcaccgc 60  
 ctcttgcccc cctgccccgc tgcccgcttg cccgcctacc cgcctacccg cctacccgcc 120  
 tccccccctg cgggcctgcc gtccttcac gcggagagcc atggagggag tgagcgcgct 180  
 gctggccccgc tgccccacgg ccggcctggc cggcggcctg ggggtcacgg cgtgcgccgc 240  
 ggccggcgctg ttgctctacc ggatcgcgcg gaggatgaag ccaacgcaca cgatgggtcaa 300  
 ctgctggttc tgcaaccagg atacgctggg gccctatggg aaccgcaact gctgggactg 360  
 tccccactgc gagcagtaca acggcttcca ggagaacggc gactacaaca agccgatccc 420  
 cgcccagtac ttggagcacc tgaaccacgt ggtgagcagc gcgcccagcc tgcgcgaccc 480  
 ttgcagccg cagcagtggg tgagcagcca agtcctgctg tgcaagaggt gcaaccacca 540  
 ccagaccacc aagatcaagc agctggccgc cttcgctccc cgcgaggagg gcaggtatga 600  
 cgaggaggtc gaggtgtacc ggcacacct ggagcagatg tacaagctgt gccggccgtg 660

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ccaagcggct gtggagtact acatcaagca ccagaaccgc cagctgcgcg ccctgttgct 720
cagccaccag ttcaagcgcc gggaggccga ccagaccac gcacagaact tctcctccgc 780
cgtgaagtcc cgggtccagg tcatcctgct ccgtgccctc gccttcctgg cctgcgctt 840
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cctggccctg ccacctggtg gcaatggctc agccacacct gacaatggca ccaccctgg 960
ggccgagggc tggcggcagt tgctgggcct actccccgag cacatggcgg agaagctgtg 1020
tgaggcctgg gcctttgggc agagccacca gacgggcgtc gtggcactgg gcctactcac 1080
ctgcctgctg gcaatgctgc tggtggccg catcaggctc cggaggatcg atgccttctg 1140
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ctcgccctagc tggtagaca cgctcaagtt cagcaccaca tctttgtgct gcctggttgg 1260
cttcacggcg gctgtggcca caaggaaggc aacggggcca cggaggttcc ggccccgaag 1320
gtcagagaag cagccatgac tgcgggggga ggacacacgg atgctcaggc ccaggctttg 1380
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ccccacccta cagccccagg tccctggcca gtccctccac tgcctcgaag agtcagtctg 1500
ccctgccttt tctttcggg caccaccagc catccccgag tgccctgtag ccactcacca 1560
ctgctgccac ctctctggcc aatggccctt tcaactggcct ggtgactgga atgtgggcag 1620
cgccacaca ggctctggcc catggcttcc tactggcagc tccaggcacc cccctctca 1679

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```

<210> 42
<211> 392
<212> PRT
<213> Homo sapiens

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<400> 42
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Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu
1           5           10          15

```

```

Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu
20           25           30

```

```

Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys
35           40           45

```

```

Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys
50           55           60

```

```

Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly
65           70           75           80

```

Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His  
85 90 95

Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln  
100 105 110

Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln  
115 120 125

Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly  
130 135 140

Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met  
145 150 155 160

Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys  
165 170 175

His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys  
180 185 190

Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val  
195 200 205

Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala  
210 215 220

Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe  
225 230 235 240

Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly  
245 250 255

Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg  
260 265 270

Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu  
275 280 285

Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly  
290 295 300

Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu  
305 310 315 320

Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly  
 325 330 335

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu  
 340 345 350

Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe  
 355 360 365

Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg  
 370 375 380

Pro Arg Arg Ser Glu Lys Gln Pro  
 385 390

<210> 43  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 43  
 ctacatcaag caccagaacc gcc 23

<210> 44  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 44  
 ggacttcacg gcggaggag 19

<210> 45  
 <211> 727  
 <212> DNA  
 <213> Homo sapiens

<400> 45  
 aggcagttgc gggttgcagg agttcaggaa aggaggtggg actagagtca acctggaata 60  
 gctctacagt aacaatggca gcctttttgt tgctgggaca tccatacagg caacttagct 120  
 ggtgaaagga ctctggattg gttggcagtc tgcttttttt tttccaaggt gatcacttta 180  
 ctgtagaaga aatgagggtta acagaaaaga gtgaggggaga acaacaactc aagcccaaca 240

actctaattgc acccaatgaa gatcaagaag aagaaatcca acagtcagaa cagcatactc 300  
cagcaaggca gcgaacacaa agagcagaca cacagccatc cagatgtcga ttgccttcac 360  
gtaggacacc tacaacatcc agcgacagaa cgatcaacct tcttgaagtc cttccgtggc 420  
ctactgagtg gattttcaac ccctatcgat tgctgtctct ttttgagctt taccctgaat 480  
ttctttctggt gtttaaagaa gccttccatg acatatccca ttgtctgaaa gccagatgg 540  
aaaagatcgg actgcccac atactccacc tcttcgcact ctccaccctc tacttctaca 600  
agtttttctt tctacaatt ctttcccttt ctttctttat tcttcttgta cttctgcttc 660  
tgctttttat tattgtcttc attctgatct tcttctgatt cttttgtttc aataaacagc 720  
aatgagc 727

<210> 46  
<211> 168  
<212> PRT  
<213> Homo sapiens  
<400> 46

Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn  
1 5 10 15

Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln Gln Ser  
20 25 30

Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln  
35 40 45

Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser  
50 55 60

Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp  
65 70 75 80

Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu  
85 90 95

Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu  
100 105 110

Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe  
115 120 125

Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu  
130 135 140

Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Phe Ile  
 145 150 155 160

Ile Val Phe Ile Leu Ile Phe Phe  
 165

<210> 47  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 47  
 gctggtgaaa ggactctgga 20

<210> 48  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 48  
 tcgctggatg ttgtaggtgt 20

<210> 49  
 <211> 950  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 gcgagcccga gcaggcagac gcgcggccgg cggctctgggg gcgcgccgcc tcccgggtccc 60  
 caaaatgtga agcggggagg gcggagacgc agagacggcc cggccggggcg ccctcgccgc 120  
 cctccggcag ccgcgccgct ccctccgctg caccgccagg cctgagcagc gagggccaccg 180  
 ggccgcgcgc tcccagcttc gctcggacgc ggcttcggcc cgcagagggg tcgtggcccg 240  
 gacgcggcga gagctggggc caggacgggtg cgtccggcct cgcgccgggc tgctcgcacc 300  
 aacaagtttg aacaatgatc accgtcaacc ccgatgggaa gataatggtc agaagatgcc 360  
 tggtcaccct gagacccttt cggctttttg tcctgggcat cggcttcttc actctctgct 420  
 tcctgatgac gtctctggga ggccagttct cggcccggcg cctgggggac tcgccattca 480  
 ccatccgcac agaagtgatg gggggccccg agtcccgcgg cgtcctgcgc aagatgagcg 540  
 acctgctgga gctgatgggt aagcgcattg acgcactggc caggctggag aacagcagtg 600

agctgcaccg ggccggcggc gacctgcact ttcccgacaga caggatgccc cctggggccg 660  
gcctcatgga gcggatccag gctattgccc agaacgtctc cgacatcgct gtgaagggtg 720  
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Thr Leu Cys Phe Leu Met Thr Ser Leu Gly Gly Gln Phe Ser Ala Arg  
35 40 45

Arg Leu Gly Asp Ser Pro Phe Thr Ile Arg Thr Glu Val Met Gly Gly  
50 55 60

Pro Glu Ser Arg Gly Val Leu Arg Lys Met Ser Asp Leu Leu Glu Leu  
65 70 75 80

Met Val Lys Arg Met Asp Ala Leu Ala Arg Leu Glu Asn Ser Ser Glu  
85 90 95

Leu His Arg Ala Gly Gly Asp Leu His Phe Pro Ala Asp Arg Met Pro  
100 105 110

Pro Gly Ala Gly Leu Met Glu Arg Ile Gln Ala Ile Ala Gln Asn Val  
115 120 125

Ser Asp Ile Ala Val Lys Val Asp Gln Ile Leu Arg His Ser Leu Leu  
130 135 140

Leu His Ser Lys Val Ser Glu Gly Arg Arg Asp Gln Cys Glu Ala Pro  
145 150 155 160



Ser Asp Pro Lys Phe Pro Asp Cys Ser Gly Lys Val Ala Val Asp Ala  
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Cys Pro Leu Asp Leu  
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<400> 54

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His Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile  
 35 40 45

Ser Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu  
 50 55 60

Asn Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val  
 65 70 75 80

Ser Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser  
 85 90 95

Glu Gln Gly

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<400> 56  
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<400> 62

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Leu Leu Thr Trp Ser Leu Phe Thr Ala Trp Leu Arg Pro Pro Thr Leu
35          40          45

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Leu Gln Gly Pro Arg Thr Ser Pro Gln Gly Ser Pro Pro Arg Ser Pro
50          55          60

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Trp Gly Asp Cys Ala Glu Pro Ser Cys Leu Cys Glu Met Lys Ile Arg
65          70          75          80

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Arg Arg Arg His Glu Gly Pro Ala Trp Gly Gln Ser Gly Phe Leu Ala
85          90          95

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Gly Gly Leu His Leu Val Pro Ser Ser Leu Ser Leu Ala Ala Cys Gly
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Val Val Arg Met Lys Gly Leu Trp Gly Arg Gly Ala Gly Ile Arg Gly
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Ser Leu Phe His Phe Ile Val Phe Ser Pro Ser Phe Leu Ser Phe Ser  
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Leu Leu Leu Ser Phe Ser Ser Leu Leu Phe Pro Leu Val Phe Asn Phe  
50 55 60

Asn Phe Asn Phe Trp Pro Ser Tyr Thr Ser Ile Cys Leu Ser Arg Lys  
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Leu Asn Ser Arg Gln Leu Ile Ile His Leu Ile Ser Ser Ala Lys Gln  
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Met Pro Ser Met Val Ser Phe Val Ile Arg Leu Leu Trp Asp Gln Asn  
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Val Ser Tyr Ser Ser Gly Lys Asn Glu Thr  
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<400> 70

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Ala Ser Leu Met Met Ile Leu Ser Ile Tyr Ser Arg Pro Leu Pro Trp  
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Ile Ile Tyr Gly Val Phe Ala Ile Leu Ser Gly Leu Val Val Leu Leu  
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Leu Pro Glu Thr Arg Asn Gln Pro Leu Leu Asp Ser Ile Gln Asp Val  
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Leu

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 35 40 45

Arg Leu Glu Cys Ser Gly Ala Ile Ser Ala Arg Cys Lys Leu Arg Leu  
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Val Gly Ser Cys His Ser Arg Ala Ser Ala Ser Gln Val Ala Gly Thr  
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Pro Thr Leu Ser Glu Lys Lys His Gln Asp Phe Leu Gly Tyr Leu Tyr  
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Arg Lys Phe Trp Phe Lys Ser Ser Lys Ala Glu Asp Glu Tyr Glu His  
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Val Gly Glu Phe Lys Gly Leu Phe Arg Ile Tyr Pro Phe Pro Glu Asn  
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Asn Ile Pro Leu Glu Lys Asp Leu Glu Ile Gln Leu Tyr Asp Phe Asp  
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Leu Phe Ser Pro Asp Asp Lys Ile Gly Thr Thr Val Ile Asp Leu Glu  
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Asn Arg Leu Leu Ser Gly Phe Gly Ala His Cys Gly Leu Ser Lys Ser  
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Phe Ser Pro Glu Glu Asp Ala Val Phe Tyr Asn Gly Lys Lys Phe Lys  
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Leu Gln Ser Phe Glu Pro Lys Thr Pro Thr Val His Gly Leu Gly Pro  
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Lys Lys Glu Arg Leu Ala Leu Tyr Leu Leu His Thr Gln Gly Leu Val  
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Pro Glu His Val Glu Thr Arg Thr Leu Tyr Ser His Ser Gln Pro Gly  
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Ile Asp Gln Gly Lys Val Gln Met Trp Val Asp Ile Phe Pro Lys Lys  
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Gly Trp Leu Tyr Gly Leu Glu Lys Asp Met Gln Lys Thr Asp Ile His  
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<210> 82  
 <211> 684  
 <212> PRT  
 <213> Homo sapiens

<400> 82

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Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu His  
 20 25 30

Leu Asp Ser Asn Arg Leu Ala Glu Val Arg Gly Asp Gln Leu Arg Gly  
 35 40 45

Leu Gly Asn Leu Arg His Leu Ile Leu Gly Asn Asn Gln Ile Arg Arg  
 50 55 60

Val Glu Ser Ala Ala Phe Asp Ala Phe Leu Ser Thr Val Glu Asp Leu  
 65 70 75 80

Asp Leu Ser Tyr Asn Asn Leu Glu Ala Leu Pro Trp Glu Ala Val Gly  
 85 90 95

Gln Met Val Asn Leu Asn Thr Leu Thr Leu Asp His Asn Leu Ile Asp  
 100 105 110

His Ile Ala Glu Gly Thr Phe Val Gln Leu His Lys Leu Val Arg Leu  
 115 120 125

Asp Met Thr Ser Asn Arg Leu His Lys Leu Pro Pro Asp Gly Leu Phe  
 130 135 140

Leu Arg Ser Gln Gly Thr Gly Pro Lys Pro Pro Thr Pro Leu Thr Val  
 145 150 155 160

Ser Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu  
 165 170 175



Arg Arg Leu Thr Arg Glu Asp Asp Leu Glu Thr Cys Ala Thr Pro Glu  
 180 185 190

His Leu Thr Asp Arg Tyr Phe Trp Ser Ile Pro Glu Glu Glu Phe Leu  
 195 200 205

Cys Glu Pro Pro Leu Ile Thr Arg Gln Ala Gly Gly Arg Ala Leu Val  
 210 215 220

Val Glu Gly Gln Ala Val Ser Leu Arg Cys Arg Ala Val Gly Asp Pro  
 225 230 235 240

Glu Pro Val Val His Trp Val Ala Pro Asp Gly Arg Leu Leu Gly Asn  
 245 250 255

Ser Ser Arg Thr Arg Val Arg Gly Asp Gly Thr Leu Asp Val Thr Ile  
 260 265 270

Thr Thr Leu Arg Asp Ser Gly Thr Phe Thr Cys Ile Ala Ser Asn Ala  
 275 280 285

Ala Gly Glu Ala Thr Ala Pro Val Glu Val Cys Val Val Pro Leu Pro  
 290 295 300

Leu Met Ala Pro Pro Pro Ala Ala Pro Pro Pro Leu Thr Glu Pro Gly  
 305 310 315 320

Ser Ser Asp Ile Ala Thr Pro Gly Arg Pro Gly Ala Asn Asp Ser Ala  
 325 330 335

Ala Glu Arg Arg Leu Val Ala Ala Glu Leu Thr Ser Asn Ser Val Leu  
 340 345 350

Ile Arg Trp Pro Ala Gln Arg Pro Val Pro Gly Ile Arg Met Tyr Gln  
 355 360 365

Val Gln Tyr Asn Ser Ser Val Asp Asp Ser Leu Val Tyr Arg Met Ile  
 370 375 380

Pro Ser Thr Ser Gln Thr Phe Leu Val Asn Asp Leu Ala Ala Gly Arg  
 385 390 395 400

Ala Tyr Asp Leu Cys Val Leu Ala Val Tyr Asp Asp Gly Ala Thr Ala  
 405 410 415

Leu Pro Ala Thr Arg Val Val Gly Cys Val Gln Phe Thr Thr Ala Gly  
 420 425 430

Asp Pro Ala Pro Cys Arg Pro Leu Arg Ala His Phe Leu Gly Gly Thr  
 435 440 445

Met Ile Ile Ala Ile Gly Gly Val Ile Val Ala Ser Val Leu Val Phe  
 450 455 460

Ile Val Leu Leu Met Ile Arg Tyr Lys Val Tyr Gly Asp Gly Asp Ser  
 465 470 475 480

Arg Arg Val Lys Gly Ser Arg Ser Leu Pro Arg Val Ser His Val Cys  
 485 490 495

Ser Gln Thr Asn Gly Ala Gly Thr Gly Ala Ala Gln Ala Pro Ala Leu  
 500 505 510

Pro Ala Gln Asp His Tyr Glu Ala Leu Arg Glu Val Glu Ser Gln Ala  
 515 520 525

Ala Pro Ala Val Ala Val Glu Ala Lys Ala Met Glu Ala Glu Thr Ala  
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Ser Ala Glu Pro Glu Val Val Leu Gly Arg Ser Leu Gly Gly Ser Ala  
 545 550 555 560

Thr Ser Leu Cys Leu Leu Pro Ser Glu Glu Thr Ser Gly Glu Glu Ser  
 565 570 575

Arg Ala Ala Val Gly Pro Arg Arg Ser Arg Ser Gly Ala Leu Glu Pro  
 580 585 590

Pro Thr Ser Ala Pro Pro Thr Leu Ala Leu Val Pro Gly Gly Ala Ala  
 595 600 605

Ala Arg Pro Arg Pro Gln Gln Arg Tyr Ser Phe Asp Gly Asp Tyr Gly  
 610 615 620

Ala Leu Phe Gln Ser His Ser Tyr Pro Arg Arg Ala Arg Arg Thr Lys  
 625 630 635 640

Arg His Arg Ser Thr Pro His Leu Asp Gly Ala Gly Gly Gly Ala Ala  
 645 650 655

Gly Glu Asp Gly Asp Leu Gly Leu Gly Ser Ala Arg Ala Cys Leu Ala  
660 665 670

Phe Thr Ser Thr Glu Trp Met Leu Glu Ser Thr Val  
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<220>  
<223> Oligonucleotide

<400> 83  
cgaactccgt gctcatc 17

<210> 84  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 84  
cgcacaaagtc gtaggca 17

<210> 85  
<211> 2206  
<212> DNA  
<213> Homo sapiens

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ccactcctcg cttctccact tcccttctcg aagtgtccgg tcgcttctcg caggcggcgc 180  
gcttgctggg tcacagtgag gcggctccgc gcaggcgag ccgggcgggc gaggagcggg 240  
gaagctgact cagggtgcg gccggggtcc tgcggggtag gagcgcgagg ccggcctgag 300  
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tatcacagtt tcagctttcc ccaaactgga atgtgtcttt gcagacgccc atccttatta 480  
aagggcaaag acttctcata cacctaggat ggatcttata ttcttggcgg gactgcagag 540  
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<210> 86  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens  
 <400> 86

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Ser Lys Leu Ala Tyr Leu Leu Ser Ser Ala Cys Leu Val Leu Ala Ala  
20 25 30

Leu Ala Ala Gly Trp Arg Val Pro Thr Pro Thr Glu Gly Gly Ser Ser  
35 40 45

Ser Pro Ser Pro Leu Thr Gln Ile Ser Val Ser Leu Gly Ala Pro Ser  
50 55 60

His Gln Lys Gln Tyr Gln Pro Ser Ser His Pro Ser Val His His His  
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Asn His Cys Leu Ile His Glu Thr Ser Ala Asp Pro Pro  
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<210> 87  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 87  
aaactacgtg tggccaggat c 21

<210> 88  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 88  
cgacatgagg actcaggaca c 21

<210> 89  
<211> 455  
<212> DNA  
<213> Homo sapiens

<400> 89  
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catgagaaca cggctctttga tggggataat tactctgaat ctaccaggct gattaagcca 120  
cagcagatca gcaggtgaga attcaactgt ccagatagaa aggtggacat ggaaaaattg 180

ggctttgcaa atgggcaccc aattcttgcc ttcttggtct ccagatcacc cttcctatac 240  
 cgccactctg gagaaagaag tacagaacgc taacaaggat ggcttggagt tgcagtggtc 300  
 acctcagatc ttaaggtcac tttggagatg gaacccctgt gactaggaat ggcagaagag 360  
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 cgtacttctg gacttccttt aaattgagag aaaca 455

<210> 90  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 90

Cys Phe Ser Gln Phe Lys Gly Ser Pro Glu Val Arg Ser Thr Gly Leu  
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Gly Trp Cys Ser Ala Thr Ser Pro Gly Leu Asn Leu Phe Leu Pro Phe  
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Ser Ser Ala Ile Pro Ser His Arg Gly Ser Ile Ser Lys Val Thr Leu  
 35 40 45

Arg Ser Glu Val Thr Thr Ala Thr Pro Ser His Pro Cys  
 50 55 60

<210> 91  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 91  
 gaacacggtc tttgatgggg 20

<210> 92  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 92  
 gccatccttg ttagcgttct g 21

<210> 93  
 <211> 1230

<212> DNA  
<213> Homo sapiens

<400> 93  
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ttgagtaccg ggagggctgc aagaccgtga ttgatgggga ggactgcgca gaccctggcg 180  
agggtgagcc cctccccgga ggcgcctgtg gaatgtccag ggctctggtc cgctcctcgg 240  
gatggggggg gcctaatacct agagccgcat tccaggataa ggggggtggg gagaggctgg 300  
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gcggggccatg gcggatgtcc ccggggcaca gcgagcgggt cctggtgacg gccagagacc 420  
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tccacgcata aataaagatt taacgaactg 1230

<210> 94  
<211> 159  
<212> PRT  
<213> Homo sapiens

<400> 94  
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Glu Pro Arg Asp Pro Leu Asp Cys Trp Ala Cys Ala Val Leu Val Thr  
20 25 30

Ala Gln Asn Leu Leu Val Ala Ala Phe Asn Leu Leu Leu Leu Val Leu  
35 40 45

Val Leu Gly Thr Ile Leu Leu Pro Ala Val Thr Met Leu Gly Phe Gly  
50 55 60

Phe Leu Cys His Ser Gln Phe Leu Arg Ser Gln Ala Pro Pro Cys Thr  
65 70 75 80

Ala His Leu Arg Asp Pro Gly Phe Thr Ala Leu Leu Val Thr Gly Phe  
85 90 95

Leu Leu Leu Val Pro Leu Leu Val Leu Ala Leu Ala Ser Tyr Arg Arg  
100 105 110

Leu Cys Leu Arg Leu Arg Leu Ala Asp Cys Leu Val Pro Tyr Ser Arg  
115 120 125

Ala Leu Tyr Arg Arg Arg Arg Ala Pro Gln Pro Arg Gln Ile Arg Ala  
130 135 140

Ser Pro Gly Ser Gln Ala Val Pro Thr Ser Gly Lys Val Trp Val  
145 150 155

<210> 95  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 95  
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<210> 96  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 96  
cgataaaggg ctcggctgta g 21

<210> 97  
<211> 1020



<212> DNA  
 <213> Homo sapiens

<400> 97  
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 cctccctaca aggaccttcc tccaagcca gggaccatgg aggaggagga ggaggatgat 180  
 gactatgaga actcaacacc tccctacaag gaccttctc ccaagccagg ttcaagtgtc 240  
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 aatcttgagc cttctccatt gcagccatcc ctggccgcaa ctccagtccc ctggctcaat 420  
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 cagtccttgg tggaaactttg gggcttatta gactgccgcc gaattacctg tcctgaaggc 660  
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 gcccggtatg tctgccagga gaattactct cacttggtca tcatcaatag ctttgctgag 780  
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 gaggaacca ataacatcca cgatgaggac tgtgctacca tgaacaaagg tggcacctgg 960  
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<210> 98  
 <211> 339  
 <212> PRT  
 <213> Homo sapiens

<400> 98  
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 Tyr Lys Asp Leu Pro Pro Lys Pro Gly Thr Met Glu Glu Glu Glu Glu  
 20 25 30  
 Asp Asp Asp Tyr Glu Asn Ser Thr Pro Pro Tyr Lys Asp Leu Pro Pro  
 35 40 45  
 Lys Pro Gly Thr Met Glu Glu Glu Glu Glu Asp Asp Asp Tyr Glu Asn  
 50 55 60

Ser Thr Pro Pro Tyr Lys Asp Leu Pro Pro Lys Pro Gly Ser Ser Ala  
 65 70 75 80  
 Pro Pro Arg Pro Pro Arg Ala Ala Lys Glu Thr Glu Lys Pro Pro Leu  
 85 90 95  
 Pro Cys Lys Pro Arg Asn Met Thr Gly Leu Asp Leu Ala Ala Val Thr  
 100 105 110  
 Cys Pro Pro Pro Gln Leu Ala Val Asn Leu Glu Pro Ser Pro Leu Gln  
 115 120 125  
 Pro Ser Leu Ala Ala Thr Pro Val Pro Trp Leu Asn Gln Arg Ser Gly  
 130 135 140  
 Gly Pro Gly Cys Cys Gln Lys Arg Trp Met Val Tyr Leu Cys Leu Leu  
 145 150 155 160  
 Val Val Thr Ser Leu Phe Leu Gly Cys Leu Gly Leu Thr Val Thr Leu  
 165 170 175  
 Ile Lys Leu Thr Gly Met Ala Gly Leu Ala Gly Leu Lys His Asp Ile  
 180 185 190  
 Ala Arg Val Arg Ala Asp Thr Asn Gln Ser Leu Val Glu Leu Trp Gly  
 195 200 205  
 Leu Leu Asp Cys Arg Arg Ile Thr Cys Pro Glu Gly Trp Leu Pro Phe  
 210 215 220  
 Glu Gly Lys Cys Tyr Tyr Phe Ser Pro Ser Thr Lys Ser Trp Asp Glu  
 225 230 235 240  
 Ala Arg Met Phe Cys Gln Glu Asn Tyr Ser His Leu Val Ile Ile Asn  
 245 250 255  
 Ser Phe Ala Glu His Asn Phe Val Ala Lys Ala His Gly Ser Pro Arg  
 260 265 270  
 Val Tyr Trp Leu Gly Leu Asn Asp Arg Ala Gln Glu Gly Asp Trp Arg  
 275 280 285  
 Trp Leu Asp Gly Ser Pro Val Thr Leu Arg Gln Pro Glu Glu Pro Asn  
 290 295 300

Asn Ile His Asp Glu Asp Cys Ala Thr Met Asn Lys Gly Gly Thr Trp  
 305 310 315 320

Asn Asp Leu Ser Cys Tyr Lys Thr Thr Tyr Trp Ile Cys Glu Arg Lys  
 325 330 335

Cys Ser Cys

<210> 99  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 99  
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<210> 100  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 100  
 aagagacact cagatatgga c 21

<210> 101  
 <211> 1680  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
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 cttctcatca ttactctcat taccctggac gtaaagctcc aaacacccat gtacttcttc 180  
 ctgaagaact tatecttttt ggatgtcttc ctggtgtctg ttccaatccc aaaattcatt 240  
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 tatgtagcca tctgctgtcc cctgaactac gaggtaatca tgaatactgg agtctgtgtg 420  
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 gcgggggactc tgttttctgg tttcagtacc acaatggaca caggcaacaa aactctgccc 780  
 caggactttc tcttactggg ctttctgggt tctcaaactc ttcagctctc tctctttatg 840  
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<210> 102  
 <211> 559  
 <212> PRT  
 <213> Homo sapiens

<400> 102

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Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile  
 20 25 30

Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr  
 35 40 45

Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu  
 50 55 60

Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile  
 65 70 75 80

Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala  
 85 90 95

Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile  
 100 105 110

Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu  
 115 120 125

Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser  
 130 135 140

Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly  
 145 150 155 160

Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe  
 165 170 175

Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met  
 180 185 190

Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys  
 195 200 205

Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu  
 210 215 220

Lys Ile Pro Thr Thr Lys Gly Leu Cys Asp Trp Val Lys Gly Leu Ser  
 225 230 235 240

Ala Gly Thr Leu Phe Ser Gly Phe Ser Thr Thr Met Asp Thr Gly Asn  
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Lys Thr Leu Pro Gln Asp Phe Leu Leu Leu Gly Phe Pro Gly Ser Gln  
 260 265 270

Thr Leu Gln Leu Ser Leu Phe Met Leu Phe Leu Val Met Tyr Ile Leu  
 275 280 285

Thr Val Ser Gly Asn Val Ala Ile Leu Met Leu Val Ser Thr Ser His  
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Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu  
 305 310 315 320

Glu Ile Trp Tyr Thr Thr Ala Ala Val Pro Lys Ala Leu Ala Ile Leu  
 325 330 335

Leu Gly Arg Ser Gln Thr Ile Ser Phe Thr Ser Cys Leu Leu Gln Met  
 340 345 350

Tyr Phe Val Phe Ser Leu Gly Cys Thr Glu Tyr Phe Leu Leu Ala Ala  
 355 360 365

Met Ala Tyr Asp Arg Cys Leu Ala Ile Cys Tyr Pro Leu His Tyr Gly  
 370 375 380

Ala Ile Met Ser Ser Leu Leu Ser Ala Gln Leu Ala Leu Gly Ser Trp  
 385 390 395 400

Val Cys Gly Phe Val Ala Ile Ala Val Pro Thr Ala Leu Ile Ser Gly  
 405 410 415

Leu Ser Phe Cys Gly Pro Arg Ala Ile Asn His Phe Phe Cys Asp Ile  
 420 425 430

Ala Pro Trp Ile Ala Leu Ala Cys Thr Asn Thr Gln Ala Val Glu Leu  
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Val Ala Phe Val Ile Ala Val Val Val Ile Leu Ser Ser Cys Leu Ile  
 450 455 460

Thr Phe Val Ser Tyr Val Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro  
 465 470 475 480

Ser Ala Ser Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser His Leu  
 485 490 495

Thr Val Val Leu Ile Trp Tyr Gly Ser Thr Val Phe Leu His Val Arg  
 500 505 510

Thr Ser Ile Lys Asp Ala Leu Asp Leu Ile Lys Ala Val His Val Leu  
 515 520 525

Asn Thr Val Val Thr Pro Val Leu Asn Pro Phe Ile Tyr Thr Leu Arg  
 530 535 540

Asn Lys Glu Val Arg Glu Thr Leu Leu Lys Lys Trp Lys Gly Lys  
 545 550 555

<210> 103  
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<220>  
 <223> Oligonucleotide

<400> 103  
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<210> 104  
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 <212> DNA  
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<220>  
 <223> Oligonucleotide

<400> 104  
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<210> 105  
 <211> 499  
 <212> DNA  
 <213> Homo sapiens

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 cctcctcacc aggggctcac tttctccaac aaaatacaac cttttggagc tcaaggagtc 180  
 ttgcatccgg aaccaggact gcgagactgg ctgctgccaa cgtgctccag acaattgcga 240  
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<210> 106  
 <211> 121  
 <212> PRT

<213> Homo sapiens

<400> 106

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Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly  
35 40 45

Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys  
50 55 60

Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr  
65 70 75 80

Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn  
85 90 95

Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg  
100 105 110

Gln Lys Leu Ala Lys Lys Met Phe Phe  
115 120

<210> 107

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 107

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17

<210> 108

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 108

ggagggagca ctagaagaac

20



<210> 109  
 <211> 659  
 <212> DNA  
 <213> Homo sapiens

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 ctcttcgga gtgggactat atgacctca tcaggccaat ccacgtcaca gaatggtcta 180  
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 ttgccagggt gcaggcatcc caggcttctt gctgccctca tgtctacaac ctgtcgtctg 300  
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 ttggtagtca ctcataaatc gtttattgca ttactaacta aataaaaaag ttgaccttg 659

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 <212> PRT  
 <213> Homo sapiens

<400> 110

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		20						25					30		

Ser	Arg	Ser	His	Phe	Tyr	His	Leu	Gln	Gln	Ser	Ser	Ser	Val	Ser	Ser
		35					40					45			

Pro	Gly	Leu	Asp	Phe	Ile	Leu	Gln	Ser	Asp	Ser	Met	Cys	Leu	Pro	Tyr
	50					55					60				

Phe	Lys	Asp	Ser	Leu	Leu	Phe	Leu	Ala	Tyr	Arg	Glu	Gln	Thr	Leu	Phe
65					70					75				80	

Phe	Ala	Phe	Leu	Val	Cys	Ser	Arg	Phe	Ser	Lys	Ile	Thr	Leu	Ser	Leu
				85					90					95	

Leu Leu Tyr Gly Ile Ile Ala Cys Asn Tyr Leu Phe Thr Tyr Leu Ser  
100 105 110

Leu Asp Trp Thr Leu Tyr Arg Gln Ala Ile Thr Asn Tyr Leu Ser Val  
115 120 125

Trp His Leu Val Val Thr His Lys Ser Phe Ile Ala Leu Leu Thr Lys  
130 135 140

<210> 111  
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<220>  
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<400> 111  
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<210> 112  
<211> 26  
<212> DNA  
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<220>  
<223> Oligonucleotide

<400> 112  
gcaaccagta aaatgtctca gcaatg 26

<210> 113  
<211> 831  
<212> DNA  
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ttcttctctga gcatgctggc tagctcaaag acagtgtaca cactgttcat cattccacag 240  
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<210> 114  
 <211> 276  
 <212> PRT  
 <213> Homo sapiens

<400> 114

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Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe Val Val Phe Leu  
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Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile Ile Met Thr Ile  
 35 40 45

Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr Phe Phe Leu Ser  
 50 55 60

Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe Ile Ile Pro Gln  
 65 70 75 80

Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile Ser Leu Ala Gly  
 85 90 95

Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala Ile Asn Asn Cys  
 100 105 110

Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met Ala Ile Cys Asn  
 115 120 125

Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val Cys Val Gln Leu  
 130 135 140

Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala Ala Val Gln Val  
 145 150 155 160

Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val Val Gly His Phe  
 165 170 175

Phe Cys Asp Ile Leu Pro Val Met Lys Leu Ser Cys Ile Asn Thr Thr  
 180 185 190

Ile Asn Glu Ile Ile Asn Phe Val Val Arg Leu Phe Val Ile Leu Val  
 195 200 205

Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser Thr Val  
 210 215 220

Leu Lys Ile Ala Ser Ala Glu Gly Trp Lys Lys Thr Phe Ala Thr Cys  
 225 230 235 240

Ala Phe His Leu Thr Val Val Ile Val His Tyr Gly Cys Ala Ser Ile  
 245 250 255

Ala Tyr Leu Met Pro Lys Ser Glu Asn Ser Ile Glu Gln Asp Leu Leu  
 260 265 270

Leu Ser Val Thr  
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<210> 115  
 <211> 18  
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<220>  
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<400> 115  
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<210> 116  
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<220>  
 <223> Oligonucleotide

<400> 116  
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<210> 117  
 <211> 1233  
 <212> DNA  
 <213> Homo sapiens

<400> 117

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<210> 118
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<212> PRT
<213> Homo sapiens

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<400> 118

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Met Ser Ile Ser Ser Leu Leu Asn Asn Thr Thr Phe Ser Thr Gly Phe
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His Lys Phe Arg Gly Lys Ser Met Asn Ile His Glu Val Thr Ile Thr
          20          25          30

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Thr Leu Thr Thr Thr Thr Ile Ile Ser Thr Ile Phe Thr Leu Leu Ile
          35          40          45

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Arg Lys Leu Pro Pro Arg Leu Pro Glu Val Thr Gln Lys Cys Ile Ser  
 50 55 60

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Tyr Pro Asp Pro Gln Leu Leu Glu Ser Cys  
 85 90

<210> 119  
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<220>  
 <223> Oligonucleotide

<400> 119  
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<210> 120  
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 <212> DNA  
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<400> 120  
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<210> 121  
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<400> 122

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Val Phe Ala Leu Gly Phe Phe Phe Leu Leu Leu Pro Tyr Leu Ser Tyr  
 35 40 45

Phe His Cys Asp Asp Pro Pro Ser Pro Ser Pro Gly Lys Arg Lys Cys  
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Pro Val Gly Arg Arg Arg Arg Pro Arg Gly Arg Met Lys Asn His Ser  
 65 70 75 80

Leu Arg Ala Gly Arg Glu Cys Pro Arg Gly Leu Glu Glu Thr Ser Asp  
 85 90 95

Leu Leu Ser Gln Leu Gln Ser Leu Leu Gly Pro His Leu Asp Lys Gly  
 100 105 110

Asp Phe Gly Gln Leu Ser Gly Pro Asp Pro Pro Gly Glu Val Gly Glu  
 115 120 125

Arg Ala Pro Asp Gly Ala Ser Gln Ser Ser His Glu Pro Met Glu Asp  
 130 135 140

Ala Ala Pro Ile Leu Ser Pro Leu Ala Ser Pro Asp Pro Gln Ala Lys  
 145 150 155 160

His Pro Gln Asp Leu Ala Ser Thr Pro Ser Pro Gly Pro Met Thr Thr  
 165 170 175

Ser Val Ser Ser Leu Ser Ala Ser Gln Pro Pro Glu Pro Ser Leu Pro  
 180 185 190

Leu Glu His Pro Ser Pro Glu Pro Pro Ala Leu Phe Pro His Pro Pro  
 195 200 205

His Thr Pro Asp Pro Leu Ala Cys Ser Pro Pro Pro Pro Lys Gly Phe  
 210 215 220

Thr Ala Pro Pro Leu Arg Asp Ser Thr Leu Ile Thr Pro Ser His Cys  
 225 230 235 240

Asp Ser Val Ala Leu Pro Leu Gly Thr Val Pro Gln Ser Leu Ser Pro  
 245 250 255

His Glu Asp Leu Val Ala Ser Val Pro Ala Ile Ser Gly Leu Gly Gly  
 260 265 270

Ser Asn Ser His Val Ser Ala Ser Ser Arg Trp Gln Glu Thr Ala Arg  
 275 280 285

Thr Ser Cys Ala Phe Asn Ser Ser Val Gln Gln Asp Pro Leu Ser Arg  
 290 295 300

His Pro Pro Glu Thr Cys Gln Met Glu Ala Gly Ser Leu Phe Leu Leu  
 305 310 315 320

Ser Ser Asp Gly Gln Asn Val Val Gly Ile Gln Val Thr Glu Thr Ala  
 325 330 335

Lys Val Asn Ile Trp Glu Glu Lys Glu Asn Val Gly Ser Phe Thr Asn  
 340 345 350

Gln Met Thr Pro Glu Lys His Leu Asn Ser Leu Gly Asn Leu Ala Lys  
 355 360 365

Ser Leu Asp Ala Glu Gln Asp Thr Thr Asn Pro Lys Pro Phe Trp Asn  
 370 375 380

Met Gly Glu Asn Ser Lys Gln Leu Pro Gly Pro Gln Lys Cys Ser Asp  
 385 390 395 400

Pro Arg Leu Leu Gln Glu Ser Phe Trp Lys Asn Tyr Ser Gln Leu Phe  
 405 410 415

Trp Gly Leu Pro Ser Leu His Ser Glu Ser Leu Val Ala Asn Ala Trp  
 420 425 430

Val Thr Asp Arg Ser Tyr Thr Leu Gln Ser Pro Pro Phe Leu Phe Asn  
 435 440 445

Glu Met Ser Asn Val Cys Pro Ile Gln Arg Glu Thr Thr Met Ser Pro  
 450 455 460

Leu Leu Phe Gln Ala Gln Pro Leu Ser His Arg Gln Pro Phe Ile Ser  
 465 470 475 480

Ser Thr Pro Gln Phe Leu Pro Thr Pro Met Ala Gln Ala Glu Ala Gln  
 485 490 495

Ala His Leu Gln Ser Ser Phe Pro Val Leu Ser Pro Ala Phe Pro Ser  
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Leu Ile Lys Asn Thr Gly Val Ala Cys Pro Ala Ser Gln Asn Lys Val  
 515 520 525

Gln Ala Leu Ser Leu Pro Glu Thr Gln His Pro Glu Trp Pro Leu Leu  
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Arg Lys Gln Leu Glu Gly Arg Leu Ala Leu Pro Ser Arg Val Gln Lys  
 545 550 555 560

Ser Gln Asp Val Phe Ser Val Ser Thr Pro Asn Leu Pro Gln Glu Ser  
 565 570 575

Leu Thr Ser Ile Leu Pro Glu Asn Phe Pro Val Ser Pro Glu Leu Arg  
 580 585 590

Arg Gln Leu Glu Gln His Ile Lys Lys Trp Ile Ile Gln His Trp Gly  
 595 600 605

Asn Leu Gly Arg Ile Gln Glu Ser Leu Asp Leu Met Gln Leu Arg Asp  
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Glu Ser Pro Gly Thr Ser Gln Ala Lys Gly Lys Pro Ser Pro Trp Gln  
 625 630 635 640

Ser Ser Thr Ser Thr Gly Glu Ser Ser Lys Glu Ala Gln Lys Val Lys  
 645 650 655

Phe Gln Leu Glu Arg Asp Leu Cys Pro His Leu Gly Gln Ile Leu Gly  
 660 665 670

Glu Thr Pro Gln Asn Leu Ser Arg Asp Met Lys Ser Phe Pro Arg Lys  
675 680 685

Val Leu Gly Val Thr Ser Glu Glu Ser Glu Arg Asn Leu Arg Lys Pro  
690 695 700

Leu Arg Ser Asp Ser Gly Ser Asp Leu Leu Arg Cys Thr Glu Arg Thr  
705 710 715 720

His Ile Glu Asn Ile Leu Lys Ala His Met Gly Arg Asn Leu Gly Gln  
725 730 735

Thr Asn Glu Gly Leu Ile Pro Val Arg Val Arg Arg Ser Trp Leu Ala  
740 745 750

Val Asn Gln Ala Leu Pro Val Ser Asn Thr His Val Lys Thr Ser Asn  
755 760 765

Leu Ala Ala Pro Lys Ser Gly Lys Ala Cys Val Asn Thr Ala Gln Val  
770 775 780

Leu Ser Phe Leu Glu Pro Cys Thr Gln Gln Gly Leu Gly Ala His Ile  
785 790 795 800

Val Arg Phe Trp Ala Lys His Arg Trp Gly Leu Pro Leu Arg Val Leu  
805 810 815

Lys Pro Ile Gln Cys Phe Lys Leu Glu Lys Val Ser Ser Leu Ser Leu  
820 825 830

Thr Gln Leu Ala Gly Pro Ser Ser Ala Thr Cys Glu Ser Gly Ala Gly  
835 840 845

Ser Glu Val Glu Val Asp Met Phe Leu Arg Lys Pro Pro Met Ala Ser  
850 855 860

Leu Arg Lys Gln Val Leu Thr Lys Ala Ser Asp His Met Pro Glu Ser  
865 870 875 880

Leu Leu Ala Ser Ser Pro Ala Trp Lys Gln Phe Gln Arg Ala Pro Arg  
885 890 895

Gly Ile Pro Ser Trp Asn Asp His Gly Pro Leu Lys Pro Pro Pro Ala  
900 905 910

Gly Gln Glu Gly Arg Trp Pro Ser Lys Pro Leu Thr Tyr Ser Leu Thr  
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Gly Ser Thr Gln Gln Ser Arg Ser Leu Gly Ala Gln Ser Ser Lys Ala  
 930 935 940

Gly Glu Thr Arg Glu Ala Val Pro Gln Cys Arg Val Pro Leu Glu Thr  
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Cys Met Leu Ala Asn Leu Gln Ala Thr Ser Glu Asp Val His Gly Phe  
 965 970 975

Glu Ala Pro Gly Thr Ser Lys Ser Ser Leu His Pro Arg Val Ser Val  
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Ser Gln Asp Pro Arg Lys Leu Cys Leu Met Glu Glu Val Val Ser Glu  
 995 1000 1005

Phe Glu Pro Gly Met Ala Thr Lys Ser Glu Thr Gln Pro Gln Val  
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Cys Ala Ala Val Val Leu Leu Pro Asp Gly Gln Ala Ser Val Val  
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Pro His Ala Ser Glu Asn Leu Val Ser Gln Val Pro Gln Gly His  
 1040 1045 1050

Leu Gln Ser Met Pro Thr Gly Asn Met Arg Ala Ser Gln Glu Leu  
 1055 1060 1065

His Asp Leu Met Ala Ala Arg Arg Ser Lys Leu Val Gln Glu Glu  
 1070 1075 1080

Pro Arg Asn Pro Asn Cys Gln Gly Ser Cys Lys Ser Gln Arg Pro  
 1085 1090 1095

Met Phe Pro Pro Ile His Lys Ser Glu Lys Ser Arg Lys Pro Asn  
 1100 1105 1110

Leu Glu Lys His Glu Glu Arg Leu Glu Gly Leu Arg Thr Pro Gln  
 1115 1120 1125

Leu Thr Pro Val Arg Lys Thr Glu Asp Thr His Gln Asp Glu Gly  
 1130 1135 1140

Val	Gln	Leu	Leu	Pro	Ser	Lys	Lys	Gln	Pro	Pro	Ser	Val	Ser	His
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1160						1165					1170			
Lys	Lys	Ser	Lys	Pro	Ala	Pro	Val	Thr	Ala	Glu	Ser	Gln	Lys	Thr
1175						1180					1185			
Val	Lys	Asn	Arg	Ser	Cys	Val	Tyr	Ser	Ser	Ser	Ala	Glu	Ala	Gln
1190						1195					1200			
Gly	Leu	Met	Thr	Ala	Val	Gly	Gln	Met	Leu	Asp	Lys	Lys	Met	Ser
1205						1210					1215			
Leu	Cys	His	Ala	His	His	Ala	Ser	Lys	Val	Asn	Gln	His	Lys	Gln
1220						1225					1230			
Lys	Phe	Gln	Ala	Pro	Val	Cys	Gly	Phe	Pro	Cys	Asn	His	Arg	His
1235						1240					1245			
Leu	Phe	Tyr	Ser	Glu	His	Gly	Arg	Ile	Leu	Ser	Tyr	Ala	Ala	Ser
1250						1255					1260			
Ser	Gln	Gln	Ala	Thr	Leu	Lys	Ser	Gln	Gly	Cys	Pro	Asn	Arg	Asp
1265						1270					1275			
Arg	Gln	Ile	Arg	Asn	Gln	Gln	Pro	Leu	Lys	Ser	Val	Arg	Cys	Asn
1280						1285					1290			
Asn	Glu	Gln	Trp	Gly	Leu	Arg	His	Pro	Gln	Ile	Leu	His	Pro	Lys
1295						1300					1305			
Lys	Ala	Val	Ser	Pro	Val	Ser	Pro	Pro	Gln	His	Trp	Pro	Lys	Thr
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Arg Arg Arg Glu Ile Ala His Val His Ala Glu Lys Gly Gln Ser Asp  
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Lys Met Asn Thr Asp Asp Leu Glu Asn Ser Ser Val Thr Ser Lys Gln  
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Thr Pro Gln Leu Val Val Ser Glu Asp Pro Met Met Met Ser Ala Val  
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Pro Ser Ala Thr Ser Leu Asn Lys Ala Phe Ser Ile Asn Lys Glu Thr  
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Gln Pro Gly Gln Ala Gly Leu Met Gln Thr Glu Arg Pro Gly Val Ser  
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Thr Pro Thr Glu Ser Gly Val Pro Ser Ala Glu Glu Val Phe Gly Ser  
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Ser Gln Pro Glu Arg Ile Ser Pro Glu Ser Gly Leu Ala Lys Ala Met  
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Leu Thr Ile Ala Ile Thr Ala Thr Pro Ser Leu Thr Val Asp Glu Lys  
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Glu Glu Leu Leu Thr Ser Thr Asn Phe Gln Pro Ile Val Glu Glu Ile  
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Thr Glu Thr Thr Lys Gly Phe Leu Lys Tyr Met Asp Asn Gln Ser Phe  
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Ala Thr Glu Ser Gln Glu Gly Val Gly Leu Gly His Ser Pro Ser Ser  
195 200 205

Tyr Val Asn Thr Lys Glu Met Leu Thr Thr Asn Pro Lys Thr Glu Lys  
210 215 220

Phe Glu Ala Asp Thr Asp His Arg Thr Thr Ser Phe Pro Gly Ala Glu  
225 230 235 240

Ser Thr Ala Gly Ser Glu Pro Gly Ser Leu Thr Pro Asp Lys Glu Lys  
245 250 255

Pro Ser Gln Met Thr Ala Asp Asn Thr Gln Ala Ala Ala Thr Lys Gln  
260 265 270

Pro Leu Glu Thr Ser Glu Tyr Thr Leu Ser Val Glu Pro Glu Thr Asp  
275 280 285

Ser Leu Leu Gly Ala Pro Glu Val Thr Val Ser Val Ser Thr Ala Val  
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Pro Ala Ala Ser Ala Leu Ser Asp Glu Trp Asp Asp Thr Lys Leu Glu  
305 310 315 320

Ser Val Ser Arg Ile Arg Thr Pro Lys Leu Gly Asp Asn Glu Glu Thr  
325 330 335

Gln Val Arg Thr Glu Met Ser Gln Thr Ala Gln Val Ser His Glu Gly  
340 345 350

Met Glu Gly Gly Gln Pro Trp Thr Glu Ala Ala Gln Val Ala Leu Gly  
355 360 365

Leu Pro Glu Gly Glu Thr His Thr Gly Thr Ala Leu Leu Ile Ala His  
370 375 380

Gly Asn Glu Arg Ser Pro Ala Phe Thr Asp Gln Ser Ser Phe Thr Pro  
385 390 395 400

Thr Ser Leu Met Glu Asp Met Lys Val Ser Ile Val Asn Leu Leu Gln  
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 485 490 495  
 Glu Lys Glu Asp Pro Ser Pro Val Ser Asp Val Pro Gly Val Thr Gln  
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 Val Pro Leu Ser Phe Glu Val Thr Pro Thr Val Glu Glu Gln Met Asp  
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Thr Leu Pro Gly Ile Thr Ser Gln Glu Pro Gly Leu Glu Glu Gly Asn  
660 665 670

Met Asp Leu Leu Glu Gly Ala Thr Tyr Gln Val Pro Asp Ala Leu Glu  
675 680 685

Trp Glu Gln Gln Asn Gln Gly Leu Val Arg Ser Trp Met Glu Lys Leu  
690 695 700

Lys Asp Lys Ala Gly Tyr Met Ser Gly Met Leu Val Pro Val Gly Val  
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Gly Ile Ala Gly Ala Leu Phe Ile Leu Gly Ala Leu Tyr Ser Ile Lys  
725 730 735

Val Met Asn Arg Arg Arg Arg Asn Gly Phe Lys Arg His Lys Arg Lys  
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Gln Arg Glu Phe Asn Ser Met Gln Asp Arg Val Met Leu Leu Ala Asp  
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18

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18

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 <212> PRT  
 <213> Homo sapiens

<400> 130

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20 25 30	

Arg Glu Lys Gln Lys Arg Asn Met Glu Glu Leu Lys Lys Glu Val Val	
35 40 45	

Met Asp Asp His Lys Leu Thr Leu Glu Glu Leu Ser Thr Lys Tyr Ser	
50 55 60	

Val Asp Leu Thr Lys Gly His Ser His Gln Arg Ala Lys Glu Ile Leu	
65 70 75 80	

Thr Arg Gly Gly Pro Asn Thr Val Thr Pro Pro Pro Thr Thr Pro Glu	
85 90 95	

Trp Val Lys Phe Cys Lys Gln Leu Phe Gly Gly Phe Ser Leu Leu Leu	
100 105 110	

Trp Thr Gly Ala Ile Leu Cys Phe Val Ala Tyr Ser Ile Gln Ile Tyr	
115 120 125	

Phe Asn Glu Glu Pro Thr Lys Asp Asn Leu Tyr Leu Ser Ile Val Leu	
130 135 140	

Ser Val Val Val Ile Val Thr Gly Cys Phe Ser Tyr Tyr Gln Glu Ala	
145 150 155 160	

Lys Ser Ser Lys Ile Met Glu Ser Phe Lys Asn Met Val Pro Gln Gln	
165 170 175	

Ala Leu Val Ile Arg Gly Gly Glu Lys Met Gln Ile Asn Val Gln Glu  
 180 185 190

Val Val Leu Gly Asp Leu Val Glu Ile Lys Gly Gly Asp Arg Val Pro  
 195 200 205

Ala Asp Leu Arg Leu Ile Ser Ala Gln Gly Cys Lys Val Asp Asn Ser  
 210 215 220

Ser Leu Thr Gly Glu Ser Glu Pro Gln Ser Arg Ser Pro Asp Phe Thr  
 225 230 235 240

His Glu Asn Pro Leu Glu Thr Arg Asn Ile Cys Phe Phe Ser Thr Asn  
 245 250 255

Cys Val Glu Gly Thr Ala Arg Gly Ile Val Ile Ala Thr Gly Asp Ser  
 260 265 270

Thr Val Met Gly Arg Ile Ala Ser Leu Thr Ser Gly Leu Ala Val Gly  
 275 280 285

Gln Thr Pro Ile Ala Ala Glu Ile Glu His Phe Ile His Leu Ile Thr  
 290 295 300

Val Val Ala Val Phe Leu Gly Val Thr Phe Phe Ala Leu Ser Leu Leu  
 305 310 315 320

Leu Gly Tyr Gly Trp Leu Glu Ala Ile Ile Phe Leu Ile Gly Ile Ile  
 325 330 335

Val Ala Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu  
 340 345 350

Thr Leu Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn  
 355 360 365

Leu Glu Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser Asp  
 370 375 380

Lys Thr Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His Met Trp  
 385 390 395 400

Phe Asp Met Thr Val Tyr Glu Ala Asp Thr Thr Glu Glu Gln Thr Gly  
 405 410 415



Lys Thr Phe Thr Lys Ser Ser Asp Thr Trp Phe Met Leu Ala Arg Ile  
420 425 430

Ala Gly Leu Cys Asn Arg Ala Asp Phe Lys Ala Asn Gln Glu Ile Leu  
435 440 445

Pro Ile Ala Lys Arg Ala Thr Thr Gly Asp Ala Ser Glu Ser Ala Leu  
450 455 460

Leu Lys Phe Ile Glu Gln Ser Tyr Ser Ser Val Ala Glu Met Arg Glu  
465 470 475 480

Lys Asn Pro Lys Val Ala Glu Ile Pro Phe Asn Ser Thr Asn Lys Tyr  
485 490 495

Gln Met Ser Ile His Leu Arg Glu Asp Ser Ser Gln Thr His Val Leu  
500 505 510

Met Met Lys Gly Ala Pro Glu Arg Ile Leu Glu Phe Cys Ser Thr Phe  
515 520 525

Leu Leu Asn Gly Gln Glu Tyr Ser Met Asn Asp Glu Met Lys Glu Ala  
530 535 540

Phe Gln Asn Ala Tyr Leu Glu Leu Gly Gly Leu Gly Glu Arg Val Leu  
545 550 555 560

Gly Phe Cys Phe Leu Asn Leu Pro Ser Ser Phe Ser Lys Gly Phe Pro  
565 570 575

Phe Asn Thr Asp Glu Ile Asn Phe Pro Met Asp Asn Leu Cys Phe Val  
580 585 590

Gly Leu Ile Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro Asp Ala  
595 600 605

Val Ser Lys Cys Arg Ser Ala Gly Ile Lys Val Ile Met Val Thr Gly  
610 615 620

Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly Val Gly Ile Ile  
625 630 635 640

Ser Glu Gly Thr Glu Thr Ala Glu Glu Val Ala Ala Arg Leu Lys Ile  
645 650 655

Pro Ile Ser Lys Val Asp Ala Ser Ala Ala Lys Ala Ile Val Val His  
660 665 670

Gly Ala Glu Leu Lys Asp Ile Gln Ser Lys Gln Leu Asp Gln Ile Leu  
675 680 685

Gln Asn His Pro Glu Ile Val Phe Ala Arg Thr Ser Pro Gln Gln Lys  
690 695 700

Leu Ile Ile Val Glu Gly Cys Gln Arg Leu Gly Ala Val Val Ala Val  
705 710 715 720

Thr Gly Asp Gly Val Asn Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile  
725 730 735

Gly Ile Ala Met Gly Ile Ser Gly Ser Asp Val Ser Lys Gln Ala Ala  
740 745 750

Asp Met Ile Leu Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val  
755 760 765

Glu Glu Gly Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Met Tyr  
770 775 780

Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Met Phe Ile  
785 790 795 800

Ile Leu Gly Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile  
805 810 815

Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ser  
820 825 830

Ala Glu Ser Asp Ile Met Lys Arg Leu Pro Arg Asn Pro Lys Thr Asp  
835 840 845

Asn Leu Val Asn His Arg Leu Ile Gly Met Ala Tyr Gly Gln Ile Gly  
850 855 860

Met Ile Gln Ala Leu Ala Gly Phe Phe Thr Tyr Phe Val Ile Leu Ala  
865 870 875 880

Glu Asn Gly Phe Arg Pro Val Asp Leu Leu Gly Ile Arg Leu His Trp  
885 890 895

Glu Asp Lys Tyr Leu Asn Asp Leu Glu Asp Ser Tyr Gly Gln Gln Trp  
 900 905 910

Thr Tyr Glu Gln Arg Lys Val Val Glu Phe Thr Cys Gln Thr Ala Phe  
 915 920 925

Phe Val Thr Ile Val Val Val Gln Trp Ala Asp Leu Ile Ile Ser Lys  
 930 935 940

Thr Arg Arg Asn Ser Leu Phe Gln Gln Gly Met Arg Asn Lys Val Leu  
 945 950 955 960

Ile Phe Gly Ile Leu Glu Glu Thr Leu Leu Ala Ala Phe Leu Ser Tyr  
 965 970 975

Thr Pro Gly Met Asp Val Ala Leu Arg Met Tyr Pro Leu Lys Ile Thr  
 980 985 990

Trp Trp Leu Cys Ala Ile Pro Tyr Ser Ile Leu Ile Phe Val Tyr Asp  
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Glu Ile Arg Lys Leu Leu Ile Arg Gln His Pro Asp Gly Trp Val  
 1010 1015 1020

Glu Arg Glu Thr Tyr Tyr  
 1025

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<220>  
 <223> Oligonucleotide

<400> 131  
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21

<210> 132  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 132  
 aagtgaagttg cggcgagt

18

<210> 133  
 <211> 279  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
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 aaagcattca gctgctccct gcctttgctc acagcgtgtg gtactctctt agaagctatt 180  
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 gcaatagaga agaaagatga tgtgaaggag agcaactga 279

<210> 134  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
 Met Tyr Val Lys Ile Ala Lys His Leu Asn Asp Val Tyr Ala Pro Gln  
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 Lys Val Leu Cys His Gly Ile Ser Tyr Ile Leu Ala Val Ile Val Ile  
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 Ile Ser His Ser Trp Ser Tyr Gly Lys Ala Phe Ser Cys Ser Leu Pro  
 35 40 45  
 Leu Leu Thr Ala Cys Gly Thr Leu Leu Glu Ala Ile Pro Val Leu Phe  
 50 55 60  
 Arg Gln Leu Phe Leu Leu Leu Val Leu Asp Leu Lys Ser Thr Gly Pro  
 65 70 75 80  
 Ala Ile Glu Lys Lys Asp Asp Val Lys Glu Ser Asn  
 85 90

<210> 135  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 135  
 tgctccctgc ctttgctcac

<210> 136  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 136  
 ggtacttggt ctcgaacgat gatc 24

<210> 137  
 <211> 1569  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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<210> 138  
<211> 522  
<212> PRT  
<213> Homo sapiens

<400> 138

Met Pro Val Gly Gly Gly Pro Glu Ser Val Gly Arg Cys Asn Gly Cys  
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Gln Cys His Ile Lys Gly Lys Gly Ile Tyr Ile Leu Asn Ser Glu Arg  
20 25 30

Pro Val Pro Gly Asp Tyr Ile Tyr Ile Arg Lys Lys Lys Gln Gln Asn  
35 40 45

Ser Asp Pro Gln Pro Lys Arg Gly Arg Gly Ser Arg Thr Ser Ala Thr  
50 55 60

Ala Asn His Ser Gly Val Leu Arg Gly Gly Ala Trp Pro Asp Asn Phe  
65 70 75 80

Gly Asp Ala Ala Gly Pro Ile Arg Thr Glu Glu Ser Glu Ala Pro Leu  
85 90 95

His Trp Ala Gln Val Arg Ser Ser Ala Ser Pro Gly Gly Gly Ala Arg  
100 105 110

Gly Met Glu Glu Ser Trp Glu Ala Ala Pro Gly Gly Gln Ala Gly Ala  
115 120 125

Glu Leu Pro Met Glu Pro Val Gly Ser Leu Val Pro Thr Leu Glu Gln  
130 135 140

Pro Gln Val Pro Ala Lys Val Arg Gln Pro Glu Gly Pro Glu Ser Ser  
145 150 155 160

Pro Ser Pro Ala Gly Ala Val Glu Lys Ala Ala Gly Ala Gly Leu Glu  
165 170 175

Pro Ser Ser Lys Lys Lys Pro Pro Ser Pro Arg Pro Gly Ser Pro Arg  
180 185 190

Val Pro Pro Leu Ser Leu Gly Tyr Gly Val Cys Pro Glu Pro Pro Ser  
195 200 205

Pro Gly Pro Ala Leu Val Lys Leu Pro Arg Asn Gly Glu Ala Pro Gly  
210 215 220

Ala Glu Pro Ala Pro Ser Ala Trp Ala Pro Met Glu Leu Gln Val Asp  
225 230 235 240

Val Arg Val Lys Pro Val Gly Ala Ala Gly Gly Ser Ser Thr Pro Ser  
245 250 255

Pro Arg Pro Ser Thr Arg Phe Leu Lys Val Pro Val Pro Glu Ser Pro  
260 265 270

Ala Phe Ser Arg His Ala Asp Pro Ala His Gln Leu Leu Leu Arg Ala  
275 280 285

Pro Ser Gln Gly Gly Thr Trp Gly Arg Arg Ser Pro Leu Ala Ala Ala  
290 295 300

Arg Thr Glu Ser Gly Cys Asp Ala Glu Gly Arg Ala Ser Pro Ala Glu  
305 310 315 320

Gly Ser Ala Gly Ser Pro Gly Ser Pro Thr Cys Cys Arg Cys Lys Glu  
325 330 335

Leu Gly Leu Glu Lys Glu Asp Ala Ala Leu Leu Pro Arg Ala Gly Leu  
340 345 350

Asp Gly Asp Glu Lys Leu Pro Arg Ala Val Thr Leu Thr Gly Leu Pro  
355 360 365

Met Tyr Val Lys Ser Leu Tyr Trp Ala Leu Ala Phe Met Ala Val Leu  
370 375 380

Leu Ala Val Ser Gly Val Val Ile Val Val Leu Ala Ser Arg Ala Gly  
385 390 395 400

Ala Arg Cys Gln Gln Cys Pro Pro Gly Trp Val Leu Ser Glu Glu His  
405 410 415

Cys Tyr Tyr Phe Ser Ala Glu Ala Gln Ala Trp Glu Ala Ser Gln Ala  
420 425 430

Phe Cys Ser Ala Tyr His Ala Thr Leu Pro Leu Leu Ser His Thr Gln  
435 440 445

Asp Phe Leu Gly Arg Tyr Pro Val Ser Arg His Ser Trp Val Gly Ala  
450 455 460

Trp Arg Gly Pro Gln Gly Trp His Trp Ile Asp Glu Ala Pro Leu Pro  
465 470 475 480

Pro Gln Leu Leu Pro Glu Asp Gly Glu Asp Asn Leu Asp Ile Asn Cys  
485 490 495

Gly Ala Leu Glu Glu Gly Thr Leu Val Ala Ala Asn Cys Ser Thr Pro  
500 505 510

Arg Pro Trp Val Cys Ala Lys Gly Thr Gln  
515 520

<210> 139  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 139  
gagaaggagg atgcggcg

18

<210> 140  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 140  
ggaccacaat gacaaccca g

21

<210> 141  
<211> 2217



<212> DNA  
<213> Homo sapiens

<400> 141

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ctgaagaaat	tattgccacg	tgttcccaaa	aacagtgtcc	tgagtgatga	aatgacaaag	180
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ctcaatgcat ggggaagcagc gattcgaaag cagtctctca gacaatctga gatggaggaa 2160  
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<210> 142  
<211> 738  
<212> PRT  
<213> Homo sapiens

<400> 142

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Glu Tyr Asn Gln Phe Gln Thr Tyr Arg Ala His Lys Ile Lys Ala Lys  
20 25 30

Arg Ser Ile Ala Thr Pro Glu Asn Leu Lys Lys Leu Leu Pro Arg Val  
35 40 45

Pro Lys Asn Ser Ala Leu Ser Asp Glu Met Thr Lys Leu His Lys Gly  
50 55 60

Ala Lys Pro Cys Lys Ser Asn Thr Phe Gly Cys Phe Pro Ile His Gln  
65 70 75 80

Ala Val Leu Ser Gly Ser Lys Glu Cys Met Glu Ile Ile Leu Lys Phe  
85 90 95

Gly Glu Glu His Gly Tyr Ser Arg Gln Cys His Ile Asn Phe Val Asp  
100 105 110

Asn Gly Lys Ala Ser Pro Leu His Leu Ala Val Gln Asn Gly Asp Leu  
115 120 125

Glu Met Met Lys Met Cys Leu Asp Asn Gly Val Gln Ile Asp Leu Val  
130 135 140

Glu Met Gln Gln Ile Lys Glu Leu Val Met Asp Glu Asp Asn Asp Gly  
 145 150 155 160

Cys Thr Pro Leu His Tyr Ala Cys Arg Gln Gly Gly Pro Gly Ser Val  
 165 170 175

Asn Asn Leu Leu Gly Phe Asn Val Ser Ile His Ser Lys Ser Lys Asp  
 180 185 190

Lys Lys Ser Pro Leu His Phe Ala Ala Ser Tyr Gly Arg Ile Asn Thr  
 195 200 205

Cys Gln Arg Leu Leu Gln Asp Ile Ser Asp Thr Arg Leu Leu Asn Glu  
 210 215 220

Gly Asp Leu His Gly Met Thr Pro Leu His Leu Ala Ala Lys Asn Gly  
 225 230 235 240

His Asp Lys Val Val Gln Leu Leu Leu Lys Lys Gly Ala Leu Phe Leu  
 245 250 255

Arg Trp Asp Glu Cys Leu Lys Val Phe Ser His Tyr Ser Pro Asn Asn  
 260 265 270

Lys Cys Pro Ile Leu Glu Met Ile Glu Tyr Leu Pro Glu Cys Met Lys  
 275 280 285

Lys Val Leu Pro Phe Phe Ser Asn Val His Val Arg Pro Ala Pro Asn  
 290 295 300

Gln Asn Gln Ile Asn His Gly Glu His Arg Leu Ala Tyr Gly Phe Ile  
 305 310 315 320

Ala His Met Ile Asn Leu Gly Phe Tyr Cys Leu Gly Leu Ile Pro Met  
 325 330 335

Thr Phe Leu Val Val Arg Ile Lys Pro Gly Met Ala Phe Asn Ser Ala  
 340 345 350

Gly Ile Ile Asn Lys Thr Ser Asp His Ser Glu Ile Leu Asp Asn Met  
 355 360 365

Asn Ser Ser Leu Ile Thr Ile Cys Met Ile Leu Val Phe Cys Ser Ser  
 370 375 380

Ile Leu Gly Tyr Val Lys Glu Val Val Gln Ile Phe Gln Gln Lys Arg  
 385 390 395 400

Asn Tyr Phe Met Asp Ile Ser Ser Ser Thr Glu Trp Ile Ile Asn Thr  
 405 410 415

Met Gly Pro Ile Leu Val Leu Pro Leu Phe Thr Glu Ile Ala Ala His  
 420 425 430

Leu Gln Phe Glu Asn Cys Gly Ile Phe Ile Val Ile Leu Glu Val Ile  
 435 440 445

Phe Lys Thr Leu Leu Arg Ser Ala Val Val Phe Phe Phe Leu Leu Leu  
 450 455 460

Ala Phe Gly Leu Ser Phe Tyr Val Leu Leu Asn Leu Gln Ser Phe Leu  
 465 470 475 480

Glu Pro Phe Leu Lys Asn Lys Leu Ala His Pro Val Leu Ser Phe Ala  
 485 490 495

Gln Leu Ile Ser Phe Thr Val Phe Ala Pro Ile Val Leu Met Asn Leu  
 500 505 510

Leu Ile Gly Leu Ala Val Gly Asp Ile Ala Glu Val Gln Lys His Ala  
 515 520 525

Ser Leu Lys Arg Ile Ala Met Gln Lys Leu Pro Cys Cys Cys Ile Arg  
 530 535 540

Lys Val Asp Arg Lys Ser Thr Ala Val Cys Pro Asn Lys Pro Arg Cys  
 545 550 555 560

Asp Gly Thr Leu Phe Gln Val Leu Leu Ala Leu Gly Pro Leu Pro Leu  
 565 570 575

Glu Glu Asn Arg Asn Ile Lys Ser Phe Leu Pro Thr Glu Ile Thr Val  
 580 585 590

Lys Arg Thr His Glu His Leu Pro Ser Ala Gly Phe Gly His His Gly  
 595 600 605

Lys His Thr Leu Ser Leu Leu Leu Val Glu Glu Trp Leu Pro Leu Asn  
 610 615 620

Val Val His Ser Ser Cys Ser Ala Phe Arg Val Val Gly Gln Ile Phe  
 625 630 635 640

Pro Ile Arg His Phe Gln Trp Ile His Val Asn Glu Pro His Thr Gly  
 645 650 655

Asn Leu Lys Glu Lys Leu Ala Ala Pro Tyr Ile Thr His Gln Ile Lys  
 660 665 670

Pro Phe Leu Arg Ala Ala Gly Phe Cys Thr Val Lys Val Val Gln Arg  
 675 680 685

Asp Asp Ile Ser Val Trp Ser Val Asp Phe Arg Trp Leu Asn Ala Trp  
 690 695 700

Glu Ala Ala Ile Arg Lys Gln Ser Leu Arg Gln Ser Glu Met Glu Glu  
 705 710 715 720

Leu Ser Cys Ser Leu Leu Leu Arg Val Thr Asp Val His Thr Arg Ser  
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Leu Tyr

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<210> 144  
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<210> 145  
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ccggacgcgg gactgaaccc gaggattcac ggagcccggt gctcccctat ggggcacggg 240  
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20 25 30

Pro Gly Arg Ala Gly Glu Cys Ala Arg Ala Gly Ala Leu Gly Gly His  
 35 40 45  
 Gly Trp Gly Ala Pro Thr Ser Gly Arg Thr Arg Asn Pro Asp Ala Gly  
 50 55 60  
 Leu Asn Pro Arg Ile His Gly Ala Arg Gly Ser Pro Met Gly His Gly  
 65 70 75 80  
 Lys Arg Gln Met Arg Val Gln Arg Gly Pro Ser His Pro Pro Pro Gly  
 85 90 95  
 Arg Leu Gly Ser Lys Ala His Arg Arg Ser Arg Leu Trp Pro Pro Pro  
 100 105 110  
 Val Gln Gln Asn Ala Gly Ser Arg Val Gly Pro Met Arg Tyr Gly Thr  
 115 120 125  
 Pro Gly Ala Ile Gly Ser Leu Ala Leu Cys Ser Gly Gly Gly Asp Pro  
 130 135 140  
 Ala Leu Lys Phe Pro Ile Thr Ser Met Asp Lys His Gly Lys Ile Met  
 145 150 155 160  
 Ser Trp Lys Asn Ser Ile Ala Leu Gln Ile Gln Thr Arg His Phe Ala  
 165 170 175  
 His Glu Thr Arg Val Pro Glu Ile Ser Arg Ser Lys Ser Arg Ile Arg  
 180 185 190  
 Asp Arg Gln Thr Tyr Gly Met Tyr His Phe Gly Asn Phe Gly Glu Glu  
 195 200 205  
 Arg Ile Lys Ala Glu Met Arg Ile Gln Lys Ala Cys His Leu Lys Ile  
 210 215 220  
 Lys Lys Ser Ser Leu Asp Ala Asn Gly Lys Val Asp Asp Gly Glu Asp  
 225 230 235 240  
 Asp Asp Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly Asp Asp Asp  
 245 250 255  
 Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly Glu Asp Asp Asp Gly  
 260 265 270

Glu Asp Asp Gly Glu Asp Asp Asp Gly Asp Asp Asp Gly Glu Asp Asp  
 275 280 285

Asp Gly Asp Asp Asp Gly Asp Asp Asp Gly Glu Asp Asp Asp Gly Glu  
 290 295 300

Asp Asp Asp Gly Asp Ser Glu Asp Asp Gly Glu Asp Gly Asp Asp Asp  
 305 310 315 320

Gly Glu Asp Asp Asp Gly Asp Ser Glu Asp Asp Gly Asp Asp Gly Asp  
 325 330 335

Asp Asp Gly Glu Asp Asp Asp His Gly Asp Asp Val Arg Met Met Met  
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<210> 149  
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<212> PRT
<213> Homo sapiens

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<400> 150

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Leu Cys Gly Gln Pro Ala Asp Tyr Leu Val Glu Glu Lys His Phe Thr
20          25          30

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Thr Leu Val Cys Phe Ile Val Val Leu Gly Gly Leu Leu Lys Met Cys
35          40          45

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Leu Lys Asn Cys Glu Val Ile Val Leu Thr Ile Leu Ser Leu Ser Gly
50          55          60

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Phe Val Ile Gly His Met Ala Tyr Asn Ser Val Glu Val His Gln Ile
65          70          75          80

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Val Tyr Pro Leu Leu Arg Thr Ser Ser Phe Ser Leu Tyr Ser Tyr Phe
85          90          95

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Ser Pro Leu Ile Ile Phe Met Val Ala Leu Asp Val Glu Phe Tyr Thr
100          105          110

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Leu Lys Lys Met Phe Trp Gln Val Leu Leu Thr Gly Leu Ile Ser Phe  
115 120 125

Ser Thr Ala Ser Ile Ile Ile Gly Tyr Val Val Ile Lys Phe Asn Lys  
130 135 140

Asp Ser Trp Asp Leu Gln Ser Cys Leu Leu Phe Ser Ile Thr Leu Gly  
145 150 155 160

Ile Ile Asp Pro Leu Arg Ser Val Asn Ser Leu Lys Thr Ile Gly Ile  
165 170 175

Ser Lys Ile Tyr Ile Asp Leu Ile Arg Gly Glu Ser Leu Ile Ile Cys  
180 185 190

Ser Ile Ala Ser Ile Phe Phe Gly Asn Phe Arg Gly Asn Arg Ile His  
195 200 205

Phe Ser Ile Phe Arg Asp Leu His Val Gly Ile Glu Leu Ser Tyr Asp  
210 215 220

Ile Leu Gly Ser Ile Ile Phe Gly Tyr Trp Cys Ala Lys Ile Ile Gln  
225 230 235 240

Cys Ile Leu Ala Asp Val Phe Ser Asn Met Leu Thr Asn Ile Ile Leu  
245 250 255

Cys Phe Ser Met Val Tyr Met Thr Phe Tyr Ile Val Glu Phe Leu Gly  
260 265 270

Met Ser Gly Thr Leu Ala Leu Ala Ala Val Gly Leu Asn Leu Asp Ser  
275 280 285

Leu Thr Phe Lys Pro Lys Ile Glu Leu Val Ile Thr Lys Phe Leu Arg  
290 295 300

Ile Phe Ser Ser Val Tyr Glu His Leu Ile Tyr Ala Phe Phe Gly Ile  
305 310 315 320

Val Ile Gly Cys Gly Glu Leu Ser His Tyr Glu Phe His Thr Ile Pro  
325 330 335

Phe Ile Phe Ile Leu Phe Thr Thr Val Asn Leu Val Arg Leu Leu Thr  
340 345 350

Ile Leu Leu Val Ser Pro Ile Leu Met His Ser Asn Tyr Glu Tyr Asn  
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Trp Arg Trp Gly Val Val Ile Thr Trp Ser Gly Ile Lys Gly Val Phe  
 370 375 380

Asn Leu Leu Trp Ala Pro Asp Val Tyr Asn Leu Ala Glu Arg Lys Val  
 385 390 395 400

Glu Val Pro Gln Met Phe Ile Leu Tyr Val Gln Val Ile Ser Leu Leu  
 405 410 415

Thr Met Gly Ile Asn Ser Tyr Val Met Thr Gln Ser Ala Arg Lys Leu  
 420 425 430

Asp Leu Cys Val Leu Ser Leu Pro Arg Gln Met Ile Leu Gln Asn Ala  
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Thr Gln His Ile Gln Glu Ile Val Gln Asn Thr Ile Thr Leu Phe Lys  
 450 455 460

Thr Glu Lys Ile Leu Thr Asn Val Asn Trp Thr Leu Val Glu Asp Lys  
 465 470 475 480

Thr Arg Ile Glu Tyr Ile Pro Phe Ser His Val Ser His Asn Asp Met  
 485 490 495

Lys Thr Glu Ser Thr Thr Asp Glu Ala Leu Met Glu Glu Ala Arg Leu  
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His Val Ala Ala Ile Gln Met Ser Ser Phe Glu Lys Gln Arg Asn Asn  
 515 520 525

Gly Ile Leu Glu Ile Glu Ala Ala Arg Ile Leu Ile Gly Ala Ala Lys  
 530 535 540

Cys Tyr Tyr Ser Ile Gln Gly Lys Phe Met Ser Ile Tyr Asp Val Ser  
 545 550 555 560

Thr Tyr Met Arg Thr Arg Ser Trp Leu Ile Lys Phe Lys Asn Val Leu  
 565 570 575

Thr Phe Leu Glu Tyr Cys Ile Glu Lys Ile His Phe Ile Pro Pro Glu  
 580 585 590

Ser Asn Thr Phe Leu Thr Phe Ile Phe His Ile Val Phe Ser Glu Glu  
595 600 605

Phe Glu Tyr Thr Gly Gln Ile Ile Asn Leu Ile Tyr Ile Tyr Pro Met  
610 615 620

Ile Ile His Leu Trp Pro Met Ala Arg Gly Leu Asn Val Ser Ala Leu  
625 630 635 640

Ile Ser Ile Asn Tyr Tyr Phe Met Phe Leu Tyr Val Leu Glu Ser Thr  
645 650 655

Leu Lys Ile Ile Ile Leu Lys Arg Lys Tyr Phe Gln Gln Cys Trp Asn  
660 665 670

Thr Leu Glu Phe Phe Ile Leu Val Ile Gly Ile Ile Asp Ile Phe Cys  
675 680 685

Val Tyr Phe Val Lys Leu Arg Pro Asp Asn Leu Ala Leu Ile Gln Leu  
690 695 700

Thr Val Ile Met Gly Tyr Leu Arg Ile Ile Arg Phe Leu Pro Leu Phe  
705 710 715 720

Lys Ile Ile Val Pro Ile Leu Ile Arg Ile Ala Asp Val Gln Ile Lys  
725 730 735

Lys Arg Leu Ser Leu Met Tyr Ser Ile Thr Lys Gly Tyr Ile Lys Ser  
740 745 750

Gln Glu Asp Ala Lys Leu Leu Ile Lys Gln Ile Ala Val Cys Glu Ser  
755 760 765

Ile Tyr Gln Lys Leu Cys Glu Ile Leu Glu Thr Asn Lys Gln Asp Ala  
770 775 780

Val Lys Glu Leu Val Leu Met Glu His Glu Gly Arg Asp Val Val Ile  
785 790 795 800

Ala Leu Lys Thr Lys Gln Ala Ile Arg Asn Val Ile Ala Lys Ala Leu  
805 810 815

Lys Asn Leu Thr Phe Leu Cys Ser Arg Gly Ile Ile Asp Lys His Glu  
820 825 830

Val Ile Glu Ile Asn Lys Val Leu Leu Lys Lys Leu Lys Ala Leu Asn  
835 840 845

Asn Phe Pro Lys Ala Ile Pro Pro Pro Thr Pro Asp Ile Tyr Leu His  
850 855 860

Asn Ile Ile Trp Leu Glu Gly Lys Asp Val Leu Ile Asp Phe Phe Lys  
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Glu Arg Ala Lys Leu Ala Cys Phe Asp Ser Gly Asp Thr Ile Cys Lys  
885 890 895

Gly Gly Glu Met Pro Gln Gly Ile Tyr Leu Ile Ile Ser Gly Met Ala  
900 905 910

Ile Leu His Ser Leu Ser Pro Thr Phe Gly Ile Glu Ser Asn Gln Arg  
915 920 925

Cys Asp Arg Gly Ser Arg Asp Met Phe Thr Glu Phe Cys Thr Thr Gly  
930 935 940

Asp Ile Ile Gly Glu Leu Ser Cys Leu Leu Lys Arg Glu Ile Glu Tyr  
945 950 955 960

Thr Val Ile Cys Glu Thr Ser Leu Gln Ala Cys Phe Ile Ser Leu Glu  
965 970 975

Asp Leu Tyr Glu Gly Phe Asp Ala Phe Trp Pro Ser Leu Glu Tyr Lys  
980 985 990

Ile Trp Leu Lys Leu Ala Leu Ser Thr Ala Tyr Gln Tyr Phe Glu Ser  
995 1000 1005

Ser Leu Ile Asp Glu Asp Leu Arg Phe Gln Asn Cys Val Met Phe  
1010 1015 1020

Asn Gln Ala Tyr Val Glu Thr Leu Ser Ser Tyr Ser Asp Met Ile  
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Ile Asp Asn Met Thr Met Lys Phe Val Ile Ile Val Tyr Gly Ser  
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Val Ile Asp Thr Lys Thr Glu Glu Pro Tyr Phe Ala Pro Cys Ile  
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Ile Pro Thr Thr Cys Glu Gln Val Gln Gly Thr Ser Asp Leu Ser  
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Lys Leu Leu Ile Ile Gln Ala Ser Glu Leu Thr Gln Arg Asn Ser  
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 tacagtcacc ctgtcaccat gccctcaaca ggcggagaca gctgtccttt ctgtctgaag 720  
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<210> 154  
 <211> 341  
 <212> PRT  
 <213> Homo sapiens

<400> 154

Met Trp Ser His Leu Asn Arg Leu Leu Phe Trp Ser Ile Phe Ser Ser  
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Glu Phe Pro Ser Pro Cys Leu Asp Ser Lys Thr Lys Val Val Met Lys  
 35 40 45

Gly Gln Asn Val Ser Met Phe Cys Ser His Lys Asn Lys Ser Leu Gln  
 50 55 60

Ile Thr Tyr Ser Leu Phe Arg Arg Lys Thr His Leu Gly Thr Gln Asp  
 65 70 75 80

Gly Lys Gly Glu Pro Ala Ile Phe Asn Leu Ser Ile Thr Glu Ala His  
 85 90 95

Glu Ser Gly Pro Tyr Lys Cys Lys Ala Gln Val Thr Ser Cys Ser Lys  
 100 105 110

Tyr Ser Arg Asp Phe Ser Phe Thr Ile Val Asp Pro Val Thr Ser Pro  
 115 120 125

Val Leu Asn Ile Met Val Ile Gln Thr Glu Thr Asp Arg His Ile Thr  
 130 135 140

Leu His Cys Leu Ser Val Asn Gly Ser Leu Pro Ile Asn Tyr Thr Phe  
 145 150 155 160

Phe Glu Asn His Val Ala Ile Ser Pro Ala Ile Ser Lys Tyr Asp Arg  
 165 170 175

Glu Pro Ala Glu Phe Asn Leu Thr Lys Lys Asn Pro Gly Glu Glu Glu  
 180 185 190

Glu Tyr Arg Cys Glu Ala Lys Asn Arg Leu Pro Asn Tyr Ala Thr Tyr  
 195 200 205

Ser His Pro Val Thr Met Pro Ser Thr Gly Gly Asp Ser Cys Pro Phe  
 210 215 220

Cys Leu Lys Leu Leu Leu Pro Gly Leu Leu Leu Leu Leu Val Val Ile  
 225 230 235 240

Ile Leu Ile Leu Ala Phe Trp Val Leu Pro Lys Tyr Lys Thr Arg Lys  
 245 250 255

Ala Met Arg Asn Asn Val Pro Arg Asp Arg Gly Asp Thr Ala Met Glu  
 260 265 270

Val Gly Ile Tyr Ala Asn Ile Leu Glu Lys Gln Ala Lys Glu Glu Ser  
 275 280 285

Val Pro Glu Val Gly Ser Arg Pro Cys Val Ser Thr Ala Gln Asp Glu  
 290 295 300

Ala Lys His Ser Gln Glu Leu Gln Tyr Ala Thr Pro Val Phe Gln Glu  
 305 310 315 320

Val Ala Pro Arg Glu Gln Glu Ala Cys Asp Ser Tyr Lys Ser Gly Tyr  
 325 330 335

Val Tyr Ser Glu Ser  
340

<210> 155  
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<220>  
<223> Oligonucleotide

<400> 155  
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<210> 156  
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<220>  
<223> Oligonucleotide

<400> 156  
acagagtgag actccatcct g 21

<210> 157  
<211> 2713  
<212> DNA  
<213> Homo sapiens

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gggggcttct atgctgctgg gctcccctag ggagttgggg tagtctgtgc caactccagg 2640  
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 tatttttgct tgt 2713

<210> 158  
 <211> 350  
 <212> PRT  
 <213> Homo sapiens

<400> 158

Met Cys Arg Cys Pro Pro Glu His His Asp Gly Arg Met Thr Ser Ala  
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Glu Val Gly Ala Ala Ala Gly Gly Ala Gln Ala Ala Gly Pro Pro Glu  
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Trp Pro Pro Gly Ser Pro Gln Ala Leu Arg Gln Pro Gly Arg Ala Arg  
 35 40 45

Val Ala Met Ala Ala Leu Val Trp Leu Leu Ala Gly Ala Ser Met Ser  
 50 55 60

Ser Leu Asn Lys Trp Ile Phe Thr Val His Gly Phe Gly Arg Pro Leu  
 65 70 75 80

Leu Leu Ser Ala Leu His Met Leu Val Ala Ala Leu Ala Cys His Arg  
 85 90 95

Gly Ala Arg Arg Pro Met Pro Gly Gly Thr Arg Cys Arg Val Leu Leu  
 100 105 110

Leu Ser Leu Thr Phe Gly Thr Ser Met Ala Cys Gly Asn Val Gly Leu  
 115 120 125

Arg Ala Val Pro Leu Asp Leu Ala Gln Leu Val Thr Thr Thr Thr Pro  
 130 135 140

Leu Phe Thr Leu Ala Leu Ser Ala Leu Leu Leu Gly Arg Arg His His  
 145 150 155 160

Pro Leu Gln Leu Ala Ala Met Gly Pro Leu Cys Leu Gly Ala Ala Cys  
 165 170 175

Ser Leu Ala Gly Glu Phe Arg Thr Pro Pro Thr Gly Cys Gly Phe Leu  
 180 185 190

Leu Ala Ala Thr Cys Leu Arg Gly Leu Lys Ser Val Gln Gln Ser Ala  
 195 200 205

Leu Leu Gln Glu Glu Arg Leu Asp Ala Val Thr Leu Leu Tyr Ala Thr  
 210 215 220

Ser Leu Pro Ser Phe Cys Leu Leu Ala Gly Ala Ala Leu Val Leu Glu  
 225 230 235 240

Ala Gly Val Ala Pro Pro Pro Thr Ala Gly Asp Ser Arg Leu Trp Ala  
 245 250 255

Cys Ile Leu Leu Ser Cys Leu Leu Ser Val Leu Tyr Asn Leu Ala Ser  
 260 265 270

Phe Ser Leu Leu Ala Leu Thr Ser Ala Leu Thr Val His Val Leu Gly  
 275 280 285

Asn Leu Thr Val Val Gly Asn Leu Ile Leu Ser Arg Leu Leu Phe Gly  
 290 295 300

Ser Arg Leu Ser Ala Leu Ser Tyr Val Gly Ile Ala Leu Thr Leu Ser  
 305 310 315 320

Gly Met Phe Leu Tyr His Asn Cys Glu Phe Val Ala Ser Trp Ala Ala  
 325 330 335

Arg Arg Gly Leu Trp Arg Arg Asp Gln Pro Ser Lys Gly Leu  
 340 345 350

<210> 159  
 <211> 21  
 <212> DNA  
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<220>  
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<400> 159  
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21

<210> 160  
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<223> Oligonucleotide

<400> 160

cctgaaagag tgagtgcgat g

21

<210> 161

<211> 963

<212> DNA

<213> Homo sapiens

<400> 161

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ttcattcctc agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 180

catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat attggttctg 240

tgggatatta ataagcgcgg tgtggaggaa actgcagctg agtgccgaaa actaggcgtc 300

actgcgcatg cgtatgtggt agactgcagc aacagagaag agatctatcg ctctctaaat 360

caggtgaaga aagaagtggg tgatgtaaca atcgtggtga ataatgctgg gacagtatat 420

ccagccgatc ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 480

ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag aaatcatggc 540

cacatcgta cagtggcttc agtgtgcggc cacgaaggga ttccttacct catcccatat 600

tgttccagca aatttgccgc tgttggcttt cacagaggtc tgacatcaga acttcaggcc 660

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acaaaaatc caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 780

ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta tatcaatatc 840

tttctgagac tacagaatcc tgataatatt aaaaacattg gtttggcact agcagcagtc 900

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tag 963

<210> 162

<211> 305

<212> PRT

<213> Homo sapiens

<400> 162

Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Ile Thr Ile Ile Tyr  
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Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys  
20 25 30

Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
35 40 45

Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln Ser Ile Leu Val  
50 55 60

Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu Thr Ala Ala Glu Cys  
65 70 75 80

Arg Lys Leu Gly Val Thr Ala His Ala Tyr Val Val Asp Cys Ser Asn  
85 90 95

Arg Glu Glu Ile Tyr Arg Ser Leu Asn Gln Val Lys Lys Glu Val Gly  
100 105 110

Asp Val Thr Ile Val Val Asn Asn Ala Gly Thr Val Tyr Pro Ala Asp  
115 120 125

Leu Leu Ser Thr Lys Asp Glu Glu Ile Thr Lys Thr Phe Glu Val Asn  
130 135 140

Ile Leu Gly His Phe Trp Ile Thr Lys Ala Leu Leu Pro Ser Met Met  
145 150 155 160

Glu Arg Asn His Gly His Ile Val Thr Val Ala Ser Val Cys Gly His  
165 170 175

Glu Gly Ile Pro Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala  
180 185 190

Val Gly Phe His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys  
195 200 205

Thr Gly Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly  
210 215 220

Phe Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp  
225 230 235 240

Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys Met  
245 250 255

Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln Asn Pro  
260 265 270



Asp Asn Ile Lys Asn Ile Gly Leu Ala Leu Ala Ala Val Lys Arg Thr  
 275 280 285

Arg Leu Ile Thr Cys Leu Pro Val Ser Gln Glu Tyr Leu Arg Ser Phe  
 290 295 300

Ser  
 305

<210> 163  
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<400> 163  
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<210> 164  
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<400> 164  
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<210> 165  
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 <212> DNA  
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 <213> Homo sapiens

<400> 166

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Leu Ser Ala Gly Val Asn Cys Thr Phe Glu Asp Leu Ser Glu Met Asp  
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Gly Leu Val Val Gly Asn Gln Ile Gln Cys Tyr Ser Pro Ala Ala Lys  
 50 55 60

Glu Val Pro Arg Ile Ile Thr Glu Asn Gly Asp His His Val Val Gln  
 65 70 75 80

Leu Gln Leu Lys Ser Lys Glu Thr Gly Met Thr Phe Ala Ser Thr Ser  
 85 90 95

Phe Val Phe Tyr Asn Cys Ser Val His Asn Ser Cys Leu Ser Cys Val  
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Glu Ser Pro Tyr Arg Cys His Trp Cys Lys Tyr Arg His Val Cys Thr  
 115 120 125

His Asp Pro Lys Thr Cys Ser Phe Gln Glu Gly Arg Val Lys Leu Pro  
 130 135 140

Glu Asp Cys Pro Gln Leu Leu Arg Val Asp Lys Ile Leu Val Pro Val  
 145 150 155 160

Glu Val Ile Lys Pro Ile Thr Leu Lys Ala Lys Asn Leu Pro Gln Pro  
 165 170 175

Gln Ser Gly Gln Arg Gly Tyr Glu Cys Ile Leu Asn Ile Gln Gly Ser  
 180 185 190

Glu Gln Arg Val Pro Ala Leu Arg Phe Asn Ser Ser Ser Val Gln Cys  
195 200 205

Gln Asn Thr Ser Tyr Ser Tyr Glu Gly Met Glu Ile Asn Asn Leu Pro  
210 215 220

Val Glu Leu Thr Val Val Trp Asn Gly His Phe Asn Ile Asp Asn Pro  
225 230 235 240

Ala Gln Asn Lys Val His Leu Tyr Lys Cys Gly Ala Met Arg Glu Ser  
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Cys Gly Leu Cys Leu Lys Ala Asp Pro Asp Phe Ala Cys Gly Trp Cys  
260 265 270

Gln Gly Pro Gly Gln Cys Thr Leu Arg Gln His Cys Pro Ala Gln Glu  
275 280 285

Ser Gln Trp Leu Glu Leu Ser Gly Ala Lys Ser Lys Cys Thr Asn Pro  
290 295 300

Arg Ile Thr Glu Ile Ile Pro Val Thr Gly Pro Arg Glu Gly Gly Thr  
305 310 315 320

Lys Val Thr Ile Arg Gly Glu Asn Leu Gly Leu Glu Phe Arg Asp Ile  
325 330 335

Ala Ser His Val Lys Val Ala Gly Val Glu Cys Ser Pro Leu Val Asp  
340 345 350

Gly Tyr Ile Pro Ala Glu Gln Ile Val Cys Glu Met Gly Glu Ala Lys  
355 360 365

Pro Ser Gln His Ala Gly Phe Val Glu Ile Cys Val Ala Val Cys Arg  
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Pro Glu Phe Met Ala Arg Ser Ser Gln Leu Tyr Tyr Phe Met Thr Leu  
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Thr Leu Ser Asp Leu Lys Pro Ser Arg Gly Pro Met Ser Gly Gly Thr  
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Gln Val Thr Ile Thr Gly Thr Asn Leu Asn Ala Gly Ser Asn Val Val  
420 425 430

Val Met Phe Gly Lys Gln Pro Cys Leu Phe His Arg Arg Ser Pro Ser  
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Tyr Ile Val Cys Asn Thr Thr Ser Ser Asp Glu Val Leu Glu Met Lys  
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Val Ser Val Gln Val Asp Arg Ala Lys Ile His Gln Asp Leu Val Phe  
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Gln Tyr Val Glu Asp Pro Thr Ile Val Arg Ile Glu Pro Glu Trp Ser  
485 490 495

Ile Val Ser Gly Asn Thr Pro Ile Ala Val Trp Gly Thr His Leu Asp  
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Leu Ile Gln Asn Pro Gln Ile Arg Ala Lys His Gly Gly Lys Glu His  
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Ile Asn Ile Cys Glu Val Leu Asn Ala Thr Glu Met Thr Cys Gln Ala  
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Pro Ala Leu Ala Leu Gly Pro Asp His Gln Ser Asp Leu Thr Glu Arg  
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Pro Glu Glu Phe Gly Phe Ile Leu Asp Asn Val Gln Ser Leu Leu Ile  
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Leu Asn Lys Thr Asn Phe Thr Tyr Tyr Pro Asn Pro Val Phe Glu Ala  
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Phe Gly Pro Ser Gly Ile Leu Glu Leu Lys Pro Gly Thr Pro Ile Ile  
595 600 605

Leu Lys Gly Lys Asn Leu Ile Pro Pro Val Ala Gly Gly Asn Val Lys  
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Leu Asn Tyr Thr Val Leu Val Gly Glu Lys Pro Cys Thr Val Thr Val  
625 630 635 640

Ser Asp Val Gln Leu Leu Cys Glu Ser Pro Asn Leu Ile Gly Arg His  
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Lys Val Met Ala Arg Val Gly Gly Met Glu Tyr Ser Pro Gly Met Val  
660 665 670

Tyr Ile Ala Pro Asp Ser Pro Leu Ser Leu Pro Ala Ile Val Ser Ile  
675 680 685

Ala Val Ala Gly Gly Leu Leu Ile Ile Phe Ile Val Ala Val Leu Ile  
690 695 700

Ala Tyr Lys Arg Lys Ser Arg Glu Ser Asp Leu Thr Leu Lys Arg Leu  
705 710 715 720

Gln Met Gln Met Asp Asn Leu Glu Ser Arg Val Ala Leu Glu Cys Lys  
725 730 735

Glu Gly Thr Glu Trp Pro His Ala Gly Gly His Val Cys Val Arg Val  
740 745 750

Cys Ile Cys Val Cys Met His Ile Cys Val Cys Val Cys Ile Cys Phe  
755 760 765

Ile Tyr Lys Gln Ala Gly Trp Ala Ala Val Gly Ser Ala Gly Gly Trp  
770 775 780

Arg Cys Val Cys Leu Cys Glu Cys Val Cys Val His Val Cys Val Cys  
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Thr Ser Val Cys Ile Tyr Val Ser Tyr Thr Ser Lys Gln Ala Gly Gln  
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<223> Oligonucleotide

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21

<210> 169

<211> 2565

<212> DNA

<213> Homo sapiens

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<212> PRT  
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<400> 170

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Phe Thr Arg Phe Asp Asn Pro Ala Ala Val Ser Pro Thr Pro Thr Arg  
35 40 45

Gln Leu Thr Phe Asn Tyr Leu Leu Pro Val Asn Ala Trp Leu Leu Leu  
50 55 60

Asn	Pro	Ser	Glu	Leu	Cys	Cys	Asp	Trp	Thr	Met	Gly	Thr	Ile	Pro	Leu	65	70	75	80
Ile	Glu	Ser	Leu	Leu	Asp	Ile	Arg	Asn	Leu	Ala	Thr	Phe	Thr	Phe	Phe	85	90	95	
Cys	Phe	Leu	Gly	Met	Leu	Gly	Val	Phe	Ser	Ile	Arg	Tyr	Ser	Gly	Asp	100	105	110	
Ser	Ser	Lys	Thr	Val	Leu	Met	Leu	Pro	Ala	Lys	Thr	Asp	Met	Gly	Gln	115	120	125	
Lys	Phe	Glu	Lys	Ser	Ser	Glu	Asp	Ser	Lys	Gln	Ser	Arg	Arg	Val	Glu	130	135	140	
Gly	Thr	Phe	Gln	Arg	Asn	Leu	Glu	Ile	Pro	Asn	Ser	Leu	Lys	Asp	Lys	145	150	155	160
Phe	Glu	Leu	Gly	Ala	His	Ala	Phe	Met	Thr	Val	Leu	Ile	Cys	Ser	Ala	165	170	175	
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Ala	Glu	Arg	Val	Leu	Tyr	Val	Pro	Ser	Met	Gly	Phe	Cys	Ile	Leu	Val	195	200	205	
Ala	His	Gly	Trp	Gln	Lys	Ile	Ser	Thr	Lys	Ser	Val	Phe	Lys	Lys	Leu	210	215	220	
Ser	Trp	Ile	Cys	Leu	Ser	Met	Val	Ile	Leu	Thr	His	Ser	Leu	Lys	Thr	225	230	235	240
Phe	His	Arg	Asn	Trp	Asp	Trp	Glu	Ser	Glu	Tyr	Thr	Leu	Phe	Met	Ser	245	250	255	
Ala	Leu	Lys	Val	Asn	Lys	Asn	Asn	Ala	Lys	Leu	Trp	Asn	Asn	Val	Gly	260	265	270	
His	Ala	Leu	Glu	Asn	Glu	Lys	Asn	Phe	Glu	Arg	Ala	Leu	Lys	Tyr	Phe	275	280	285	
Leu	Gln	Ala	Thr	His	Val	Gln	Pro	Asp	Asp	Ile	Gly	Ala	His	Met	Asn	290	295	300	

Val Gly Arg Thr Tyr Lys Asn Leu Asn Arg Thr Lys Glu Ala Glu Glu  
 305 310 315 320

Ser Tyr Met Met Ala Lys Ser Leu Met Pro Gln Ile Ile Pro Gly Lys  
 325 330 335

Lys Tyr Ala Ala Arg Ile Ala Pro Asn His Leu Asn Val Tyr Ile Asn  
 340 345 350

Leu Ala Asn Leu Ile Arg Ala Asn Glu Ser Arg Leu Glu Glu Ala Asp  
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Gln Leu Tyr Arg Gln Ala Ile Ser Met Arg Pro Asp Phe Lys Gln Ala  
 370 375 380

Tyr Ile Ser Arg Gly Glu Leu Leu Leu Lys Met Asn Lys Pro Leu Lys  
 385 390 395 400

Ala Lys Glu Ala Tyr Leu Lys Ala Leu Glu Leu Asp Arg Asn Asn Ala  
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Asp Leu Trp Tyr Asn Leu Ala Ile Val His Ile Glu Leu Lys Glu Pro  
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Asn Glu Ala Leu Lys Asn Phe Asn Arg Ala Leu Glu Leu Asn Pro Lys  
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His Lys Leu Ala Leu Phe Asn Ser Ala Ile Val Met Gln Glu Ser Gly  
 450 455 460

Glu Val Lys Leu Arg Pro Glu Ala Arg Lys Arg Leu Leu Ser Tyr Ile  
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Asn Glu Glu Pro Leu Asp Ala Asn Gly Tyr Phe Asn Leu Gly Met Leu  
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Ala Met Asp Asp Lys Lys Asp Asn Glu Ala Glu Ile Trp Met Lys Lys  
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Ala Ile Lys Leu Gln Ala Asp Phe Arg Ser Ala Leu Phe Asn Leu Ala  
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Leu Leu Tyr Ser Gln Thr Ala Lys Glu Leu Lys Ala Leu Pro Ile Leu  
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Glu Glu Leu Leu Arg Tyr Tyr Pro Asp His Ile Lys Gly Leu Ile Leu  
 545 550 555 560

Lys Gly Asp Ile Leu Met Asn Gln Lys Lys Asp Ile Leu Gly Ala Lys  
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Lys Cys Phe Glu Arg Ile Leu Glu Met Asp Pro Ser Asn Val Gln Gly  
 580 585 590

Lys His Asn Leu Cys Val Val Tyr Phe Glu Glu Lys Asp Leu Leu Lys  
 595 600 605

Ala Glu Arg Cys Leu Leu Glu Thr Leu Ala Leu Ala Pro His Glu Glu  
 610 615 620

Tyr Ile Gln Arg His Leu Asn Ile Val Arg Asp Lys Ile Ser Ser Ser  
 625 630 635 640

Ser Phe Ile Glu Pro Ile Phe Pro Thr Ser Lys Ile Ser Ser Val Glu  
 645 650 655

Gly Lys Lys Ile Pro Thr Glu Ser Val Lys Glu Ile Arg Gly Glu Ser  
 660 665 670

Arg Gln Thr Gln Ile Val Lys Thr Ser Asp Asn Lys Ser Gln Ser Lys  
 675 680 685

Ser Asn Lys Gln Leu Gly Lys Asn Gly Asp Glu Glu Thr Pro His Lys  
 690 695 700

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Lys Arg Leu Glu Glu Ile Glu Arg Ile Leu Asn Gly Glu  
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<212> PRT  
<213> Homo sapiens

<400> 174

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Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr  
35 40 45

Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr  
50 55 60

Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu  
65 70 75 80

Ala Ala Leu Val Leu Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val  
85 90 95

Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu  
100 105 110

Ala Ser Phe Thr Tyr Leu Ser Phe Ser Ala Leu Ala His Leu Leu Gln  
115 120 125

Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Phe Leu Asp Tyr Val  
130 135 140

Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr  
145 150 155 160

Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro  
165 170 175



Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn  
180 185 190

Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val  
195 200 205

Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg  
210 215 220

Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr  
225 230 235 240

His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Ala Phe Phe Ser  
245 250 255

Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly  
260 265 270

Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala  
275 280 285

Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr  
290 295 300

Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu  
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Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu  
325 330 335

Val Gln Arg Lys Leu Asp Gln Lys Thr Lys  
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 <211> 501  
 <212> PRT  
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<400> 176

Met Arg Ser Ser Leu Ala Pro Gly Val Trp Phe Phe Arg Ala Phe Ser  
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Arg Asp Ser Trp Phe Arg Gly Leu Ile Leu Leu Leu Thr Phe Leu Ile  
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Tyr Ala Cys Tyr His Met Ser Arg Lys Pro Ile Ser Ile Val Lys Ser  
 35 40 45

Arg Leu His Gln Asn Cys Ser Glu Gln Ile Lys Pro Ile Asn Asp Thr  
 50 55 60

His Ser Leu Asn Asp Thr Met Trp Cys Ser Trp Ala Pro Phe Asp Lys  
 65 70 75 80

Asp Asn Tyr Lys Glu Leu Leu Gly Gly Val Asp Asn Ala Phe Leu Ile  
 85 90 95

Ala Tyr Ala Ile Gly Met Phe Ile Ser Gly Val Phe Gly Glu Arg Leu  
 100 105 110

Pro Leu Arg Tyr Tyr Leu Ser Ala Gly Met Leu Leu Ser Gly Leu Phe  
 115 120 125

Thr Ser Leu Phe Gly Leu Gly Tyr Phe Trp Asn Ile His Glu Leu Trp  
 130 135 140

Tyr Phe Val Val Ile Gln Val Cys Asn Gly Leu Val Gln Thr Thr Gly  
 145 150 155 160

Trp Pro Ser Val Val Thr Cys Val Gly Asn Trp Phe Gly Lys Gly Lys  
 165 170 175

Arg Gly Phe Ile Met Gly Ile Trp Asn Ser His Thr Ser Val Gly Asn  
 180 185 190

Ile Leu Gly Ser Leu Ile Ala Gly Ile Trp Val Asn Gly Gln Trp Gly  
 195 200 205

Leu Ser Phe Ile Val Pro Gly Ile Ile Thr Ala Val Met Gly Val Ile  
 210 215 220

Thr Phe Leu Phe Leu Ile Glu His Pro Glu Asp Val Asp Cys Ala Pro  
 225 230 235 240

Pro Gln His His Gly Glu Pro Ala Glu Asn Gln Asp Asn Pro Glu Asp  
 245 250 255

Pro Gly Asn Ser Pro Cys Ser Ile Arg Glu Ser Gly Leu Glu Thr Val  
 260 265 270

Ala Lys Cys Ser Lys Gly Pro Cys Glu Glu Pro Ala Ala Ile Ser Phe  
 275 280 285

Phe Gly Ala Leu Arg Ile Pro Gly Val Val Glu Phe Ser Leu Cys Leu  
 290 295 300

Leu Phe Ala Lys Leu Val Ser Tyr Thr Phe Leu Tyr Trp Leu Pro Leu  
 305 310 315 320

Tyr Ile Ala Asn Val Ala His Phe Ser Ala Lys Glu Ala Gly Asp Leu  
 325 330 335

Ser Thr Leu Phe Asp Val Gly Gly Ile Ile Gly Gly Ile Val Ala Gly  
 340 345 350

Leu Val Ser Asp Tyr Thr Asn Gly Arg Ala Thr Thr Cys Cys Val Met  
 355 360 365

Leu Ile Leu Ala Ala Pro Met Met Phe Leu Tyr Asn Tyr Ile Gly Gln  
 370 375 380

Asp Gly Ile Ala Ser Ser Ile Val Met Leu Ile Ile Cys Gly Gly Leu  
 385 390 395 400

Val Asn Gly Pro Tyr Ala Leu Ile Thr Thr Ala Val Ser Ala Asp Leu  
 405 410 415

Gly Thr His Lys Ser Leu Lys Gly Asn Ala Lys Ala Leu Ser Thr Val  
 420 425 430

Thr Ala Ile Ile Asp Gly Thr Gly Ser Ile Gly Ala Ala Leu Gly Pro  
 435 440 445

Leu Leu Ala Gly Leu Ile Ser Pro Thr Gly Trp Asn Asn Val Phe Tyr  
 450 455 460

Met Leu Ile Ser Ala Asp Val Leu Ala Cys Leu Leu Leu Cys Arg Leu  
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Val Tyr Lys Glu Ile Leu Ala Trp Lys Val Ser Leu Ser Arg Gly Ser  
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Gly Tyr Lys Glu Ile  
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<400> 178  
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<210> 179  
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 <212> DNA  
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 <213> Homo sapiens

<400> 180

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Ala Ile Phe Cys Ser Ser Leu Leu Asp Ser Val Pro Gln Lys Val Glu  
 35 40 45

Phe Phe Ile Asn Tyr Ser Ser Trp Gly Leu Met Pro Val Gly Phe Asp  
 50 55 60

Gln Trp Val Thr Pro Ser Val Asp Trp Arg Met Glu Lys Glu Lys Arg  
 65 70 75 80

Leu Gly Tyr Val Ser Pro Pro Leu Phe Leu Leu Leu Ala Gly Phe  
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<400> 181  
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<210> 182  
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<220>  
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<400> 182  
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<210> 183  
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 <212> DNA  
 <213> Homo sapiens

<400> 183

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<210> 184
<211> 166
<212> PRT
<213> Homo sapiens

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<400> 184

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Ser Gln Glu Phe Pro Ala His Glu Gly Arg Gly Asp Glu Glu Arg Pro
20          25          30

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Ile Asp Val Arg Val Val Gln Ala Ala Pro Leu Arg Cys Asp Ser Thr
35          40          45

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Pro Pro Glu Gly Ala Val Gly Asp Ile Cys Lys Lys Glu Asp Ala Gly
50          55          60

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Asn Met Pro Ser Thr Ser Glu Gly Ser Ile Tyr Pro Glu Met Ala His
65          70          75          80

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Phe Leu Arg Asn Lys Leu Ala Gly Ser Ser Val Arg Lys Pro Asp Ser
85          90          95

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Gly Phe Leu Trp Glu Gly Ala Leu Arg Ala Trp Leu Phe Leu Ile Leu
100          105          110

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Ile Val Leu Thr His Ile Met Trp Val Pro Leu Val Gln Val Ser Pro
115          120          125

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Asn Ala Pro Leu Phe His Tyr Ile Glu Ser Ile Ala His Asp Leu Gly
130          135          140

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Lys Glu Pro Met Ser Arg  
 165

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Asn Arg His Leu Glu Asp Phe Pro Ile Pro Val Pro Val Ile Leu Phe  
35 40 45

Leu Leu Gly Cys Ser Phe Glu Val Leu Ser Phe Thr Ser Ser Gln Val  
50 55 60

Gln Arg Tyr Ala Asn Ala Ile Gln Trp Met Ser Pro Asp Leu Phe Phe  
65 70 75 80

Arg Ile Phe Thr Pro Val Val Phe Phe Thr Thr Ala Phe Asp Met Asp  
85 90 95

Thr Tyr Met Leu Gln Lys Leu Phe Trp Gln Ile Leu Leu Ile Ser Ile  
100 105 110

Pro Gly Phe Leu Val Asn Tyr Ile Leu Val Leu Trp His Leu Ala Ser  
115 120 125

Val Asn Gln Leu Leu Leu Lys Pro Thr Gln Trp Leu Leu Phe Ser Ala  
130 135 140

Ile Leu Val Ser Ser Asp Pro Met Leu Thr Ala Ala Ala Ile Arg Asp  
145 150 155 160

Leu Gly Leu Ser Arg Ser Leu Ile Ser Leu Ile Asn Gly Glu Ser Leu  
165 170 175

Met Thr Ser Val Ile Ser Leu Ile Thr Phe Thr Ser Ile Met Asp Phe  
180 185 190

Asp Gln Arg Leu Gln Ser Lys Arg Asn His Thr Leu Ala Glu Glu Ile  
195 200 205

Val Gly Gly Ile Cys Ser Tyr Ile Ile Ala Ser Phe Leu Phe Gly Ile  
210 215 220

Leu Ser Ser Lys Leu Ile Gln Phe Trp Met Ser Thr Val Phe Gly Asp  
225 230 235 240

Asp Val Asn His Ile Ser Leu Ile Phe Ser Ile Leu Tyr Leu Ile Phe  
245 250 255

Tyr Ile Cys Glu Leu Val Gly Met Ser Gly Ile Phe Thr Leu Ala Ile  
260 265 270

Val Gly Leu Leu Leu Asn Ser Thr Ser Phe Lys Ala Ala Ile Glu Glu  
275 280 285

Thr Leu Leu Leu Glu Phe Leu Thr Leu Leu Leu Ile Ser Pro Val Leu  
290 295 300

Ser Arg Val Gly His Glu Phe Ser Trp Arg Trp Ile Phe Ile Met Val  
305 310 315 320

Cys Ser Glu Met Lys Gly Met Pro Asn Ile Asn Met Ala Leu Leu Leu  
325 330 335

Ala Tyr Ser Asp Leu Tyr Phe Gly Ser Asp Lys Glu Lys Ser Gln Ile  
340 345 350

Leu Phe His Gly Val Leu Val Cys Leu Ile Thr Leu Val Val Asn Arg  
355 360 365

Phe Ile Leu Pro Val Ala Val Thr Ile Leu Gly Leu Arg Asp Ala Thr  
370 375 380

Ser Thr Lys Tyr Lys Ser Val Cys Cys Thr Phe Gln His Phe Gln Glu  
385 390 395 400

Leu Thr Lys Ser Ala Ala Ser Ala Leu Lys Phe Asp Lys Asp Leu Ala  
405 410 415

Asn Ala Asp Trp Asn Met Ile Glu Lys Ala Ile Thr Leu Glu Asn Pro  
420 425 430

Tyr Met Leu Asn Glu Glu Glu Thr Thr Glu His Gln Lys Val Lys Cys  
435 440 445

Pro His Cys Asn Lys Glu Ile Asp Glu Ile Phe Asn Thr Glu Ala Met  
450 455 460

Glu Leu Ala Asn Arg Arg Leu Leu Ser Ala Gln Ile Ala Ser Tyr Gln  
465 470 475 480

Arg Gln Tyr Arg Asn Glu Ile Leu Ser Gln Ser Ala Val Gln Val Leu  
485 490 495

Val Gly Ala Ala Glu Ser Phe Gly Glu Lys Lys Gly Lys Cys Met Ser  
500 505 510

Leu Asp Thr Ile Lys Asn Tyr Ser Glu Ser Gln Lys Thr Val Thr Phe  
515 520 525

Ala Arg Lys Leu Leu Leu Asn Trp Val Tyr Asn Thr Arg Lys Glu Lys  
530 535 540

Glu Gly Pro Ser Lys Tyr Phe Phe Phe Arg Ile Cys His Thr Ile Val  
545 550 555 560

Phe Thr Glu Glu Phe Glu His Val Gly Tyr Leu Val Ile Leu Met Asn  
565 570 575

Ile Phe Pro Phe Ile Ile Ser Trp Ile Ser Gln Leu Asn Val Ile Tyr  
580 585 590

His Ser Glu Leu Lys His Thr Asn Tyr Cys Phe Leu Thr Leu Tyr Ile  
595 600 605

Leu Glu Ala Leu Leu Lys Ile Ala Ala Met Arg Lys Asp Phe Phe Ser  
610 615 620

His Ala Trp Asn Ile Phe Glu Leu Ala Ile Thr Leu Ile Gly Ile Leu  
625 630 635 640

His Val Ile Leu Ile Glu Ile Asp Thr Ile Lys Tyr Ile Phe Asn Glu  
645 650 655

Thr Glu Val Ile Val Phe Ile Lys Val Val Gln Phe Phe Arg Ile Leu  
660 665 670

Arg Ile Phe Lys Leu Ile Ala Pro Lys Leu Leu Gln Ile Ile Asp Lys  
675 680 685

Arg Met Ser His Gln Lys Thr Phe Trp Tyr Gly Ile Leu Lys Gly Tyr  
690 695 700

Val Gln Gly Glu Ala Asp Ile Met Thr Ile Ile Asp Gln Ile Thr Ser  
705 710 715 720



Ser Lys Gln Ile Lys Gln Met Leu Leu Lys Gln Val Ile Arg Asn Met  
725 730 735

Glu His Ala Ile Lys Glu Leu Gly Tyr Leu Glu Tyr Asp His Pro Glu  
740 745 750

Ile Ala Val Thr Val Lys Thr Lys Glu Glu Ile Asn Val Met Leu Asn  
755 760 765

Met Ala Thr Glu Ile Leu Lys Ala Phe Gly Leu Lys Gly Ile Ile Ser  
770 775 780

Lys Thr Glu Gly Ala Gly Ile Asn Lys Leu Ile Met Ala Lys Lys Lys  
785 790 795 800

Glu Val Leu Asp Ser Gln Ser Ile Ile Arg Pro Leu Thr Val Glu Glu  
805 810 815

Val Leu Tyr His Ile Pro Trp Leu Asp Lys Asn Lys Asp Tyr Ile Asn  
820 825 830

Phe Ile Gln Glu Lys Ala Lys Val Val Thr Phe Asp Cys Gly Asn Asp  
835 840 845

Ile Phe Glu Glu Gly Asp Glu Pro Lys Gly Ile Tyr Ile Ile Ile Ser  
850 855 860

Gly Met Val Lys Leu Glu Lys Ser Lys Pro Gly Leu Gly Ile Asp Gln  
865 870 875 880

Met Val Glu Ser Lys Glu Lys Asp Phe Pro Ile Ile Asp Thr Asp Tyr  
885 890 895

Met Leu Ser Gly Glu Ile Ile Gly Glu Ile Asn Cys Leu Thr Asn Glu  
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Pro Met Lys Tyr Ser Ala Thr Cys Lys Thr Val Val Glu Thr Cys Phe  
915 920 925

Ile Pro Lys Thr His Leu Tyr Asp Ala Phe Glu Gln Cys Ser Pro Leu  
930 935 940

Ile Lys Gln Lys Met Trp Leu Lys Leu Gly Leu Ala Ile Thr Ala Arg  
945 950 955 960

Lys Ile Arg Glu His Leu Ser Tyr Glu Asp Trp Asn Tyr Asn Met Gln  
 965 970 975

Leu Lys Leu Ser Asn Ile Tyr Val Val Asp Ile Pro Met Ser Thr Lys  
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Thr Asp Ile Tyr Asp Glu Asn Leu Ile Tyr Val Ile Leu Ile His Gly  
 995 1000 1005

Ala Val Glu Asp Cys Leu Leu Arg Lys Thr Tyr Arg Ala Pro Phe  
 1010 1015 1020

Leu Ile Pro Ile Thr Cys His Gln Ile Gln Ser Ile Glu Asp Phe  
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Thr Lys Val Val Ile Ile Gln Thr Pro Ile Asn Met Lys Thr Phe  
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Arg Arg Asn Ile Arg Lys Phe Val Pro Lys His Lys Ser Tyr Leu  
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Thr Pro Gly Leu Ile Gly Ser Val Gly Thr Leu Glu Glu Gly Ile  
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Gln Glu Glu Arg Asn Val Lys Glu Asp Gly Ala His Ser Ala Ala  
 1085 1090 1095

Thr Ala Arg Ser Pro Gln Pro Cys Ser Leu Leu Gly Thr Lys Phe  
 1100 1105 1110

Asn Cys Lys Glu Ser Pro Arg Ile Asn Leu Arg Lys Val Arg Lys  
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<400> 192

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 35 40 45

Met Lys Tyr Phe Lys Phe Asn Ile Ser Leu Ala Asn Ala Glu Phe Ile  
 50 55 60

Ser Gln Asp Ser Trp Leu Ala Trp Val Gly Phe Val Lys Val Val Lys  
 65 70 75 80

Tyr Lys Ala Tyr Cys Lys Arg Tyr Gln Val Thr Phe Arg Arg Gln Cys  
 85 90 95

Glu Gly Lys Thr Asp Tyr Tyr Ala Trp Lys His Leu Val Val Gln Asp  
 100 105 110

Lys Asn Lys Ser Asn Thr His Lys Tyr Arg Met Ile Ile Cys Val Ile  
 115 120 125

Asn Thr Asp Thr Ile Cys Glu Met Ala Tyr Ala His Ile Glu Trp Asp  
 130 135 140

Met Ile Val Cys Ala Ala Tyr Ala His Glu Leu Pro Lys Tyr Gly Val  
 145 150 155 160

Lys Val Gly Leu Thr Asn Asp Ala Ala Ala Cys Cys Thr Gly Leu Leu  
 165 170 175

Leu Ala Cys Arg Leu Leu Ser Arg Phe Gly Met Asp Lys Ile Tyr Lys  
 180 185 190

Gly Gln Val Glu Val Thr Arg Asp Glu Tyr Asn Val Gly Ser Thr Asp  
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Gly Gln Pro Gly Ala Phe Thr Cys Cys Leu Asp Ala Gly Leu Ala Arg  
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Thr Thr Thr Asp Asn Lys Val Phe Gly Ala Leu Arg Val Leu Trp Met  
 225 230 235 240

Glu Val Ser Leu Ser Leu Thr Val Pro Asn Asp Ser Leu Ser Lys Gly  
 245 250 255

Lys Pro Gly Pro Arg Lys Glu Gln Leu Pro Ala Arg Gly Ser Leu Ser  
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Arg Gly Val Leu Gly Ala Phe Glu Val Gly Ser Gln Gly Val Glu Ala  
 275 280 285

Ala Ala Ser Pro Asn Gly Gln Tyr Gly Pro Ser Trp Gly Leu Ala Ala  
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Glu Gly Thr Glu Gly Ala Arg Pro Gln Ala Pro Lys Arg Asp Leu Ser  
 305 310 315 320

Tyr Ser Arg Thr Asp Ser His Arg Asp Cys Ser Pro Val Cys His Asn  
 325 330 335

Met Ser Leu Arg Gly His Leu Val Pro Lys Lys Pro Ser Lys Glu Lys  
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Gln Gly Gln Gln Lys Leu Asp Ser Lys Phe Tyr Glu Ser Trp Ala Thr  
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Ala Leu Leu Thr Ala Ile Phe Pro Val Leu Gly Ile Leu Val Leu Val  
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 385 390 395 400

Ser Gly Phe Ser Gly Pro Arg Ala Arg Leu Leu Gly Val Leu Ala Leu  
 405 410 415

Gly Gly Leu Pro Leu His Leu Gly Ala Pro Val Ile Val Met Ala Trp  
 420 425 430

Ile Val Leu Ala Leu Leu Phe Thr Arg Ser Arg Thr Arg Ala Asp Pro  
 435 440 445

Ala Asp Val Leu Pro Pro Gly Ala Phe Glu Lys Thr Arg Met His Ala  
 450 455 460

Leu Pro Pro Pro Leu Gly Leu Thr Leu Asp Asp Gly Glu Val Ile Thr  
 465 470 475 480

Thr Arg Leu Leu Thr Asp Ala Ser Val Gln Lys Val Val Val Arg Ile  
 485 490 495

Ser Glu Ser Ser Ser Cys Leu His Asn Gly Leu Leu Ser Gly Asn Gly  
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Cys Glu Val His Tyr Arg Arg Ala Arg Leu Phe Gln Asp Ala Gln Met  
 515 520 525

Pro Ala Gln Ser Pro Ala Tyr Arg Gly Asp Leu Arg Ala Pro Val Asn  
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Ala Leu Arg Ile Gln Asn Arg Ser Gln Leu Ser Pro Gly Gly Lys Ile  
 545 550 555 560

Lys Trp Arg Gln His Arg Gln Leu Glu Gly Thr His Arg Lys Lys Ser  
 565 570 575

Ser Thr Met Phe Arg Lys Ile His Ser Ile Phe Asn Ser Ser Pro Gln  
 580 585 590

Arg Lys Thr Ala Ala Glu Ser Pro Phe Tyr Glu Gly Ala Ser Pro Ala  
 595 600 605

Val Lys Leu Ile Arg Ser Ser Ser Met Tyr Val Val Gly Asp His Gly  
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Glu Lys Phe Ser Glu Ser Leu Lys Lys Tyr Lys Ser Thr Ser Ser Met  
 625 630 635 640

Asp Thr Ser Leu Tyr Tyr Leu Arg Gln Glu Glu Asp Arg Ala Trp Met  
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Tyr Ser Arg Thr Gln Asp Cys Leu Gln Tyr Leu Gln Glu Leu Leu Ala  
 660 665 670

Leu Arg Lys Lys Tyr Leu Ser Ser Phe Ser Asp Leu Lys Pro His Arg  
 675 680 685

Thr Gln Gly Ile Ser Ser Thr Ser Ser Lys Ser Ser Lys Gly Gly Lys  
 690 695 700

Lys Thr Pro Val Arg Ser Thr Pro Lys Glu Ile Lys Lys Ala Thr Pro  
705 710 715 720

Lys Lys Tyr Ser Gln Phe Ser Ala Asp Val Ala Glu Ala Ile Ala Phe  
725 730 735

Phe Asp Ser Ile Ile Ala Glu Leu Asp Thr Glu Arg Arg Pro Arg Ala  
740 745 750

Ala Glu Ala Ser Leu Pro Asn Glu Asp Val Asp Phe Asp Val Ala Thr  
755 760 765

Ser Ser Arg Glu His Ser Leu His Ser Asn Trp Ile Leu Arg Ala Pro  
770 775 780

Arg Arg His Ser Glu Asp Ile Ala Ala His Thr Val His Thr Val Asp  
785 790 795 800

Gly Gln Phe Arg Arg Ser Thr Glu His Arg Thr Val Gly Thr Gln Arg  
805 810 815

Arg Leu Glu Arg His Pro Ile Tyr Leu Pro Lys Ala Val Glu Gly Ala  
820 825 830

Phe Asn Thr Trp Lys Phe Lys Pro Lys Ala Cys Lys Lys Asp Leu Gly  
835 840 845

Ser Ser Arg Gln Ile Leu Phe Asn Phe Ser Gly Glu Asp Met Glu Trp  
850 855 860

Asp Ala Glu Leu Phe Ala Leu Glu Pro Gln Leu Ser Pro Gly Glu Asp  
865 870 875 880

Tyr Tyr Glu Thr Glu Asn Pro Lys Gly Gln Trp Leu Leu Arg Glu Arg  
885 890 895

Leu Trp Glu Arg Thr Thr Gly Ser Leu Arg Ser Cys Pro Leu Ser Ala  
900 905 910

Gln His Glu Val Phe Gly Arg Val Glu Asn Ala Asn Cys Asn Thr Val  
915 920 925

Asn Pro Leu Ser Thr Leu Pro Ala Gly Ala Val Pro Val Pro Asn Arg  
930 935 940



Pro Val Ala Ser Gln Gly Thr Gly Leu Arg Thr Leu Ser Glu Leu Glu  
 945 950 955 960

Phe Leu Cys Val Gly  
 965

<210> 193  
 <211> 22  
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<220>  
 <223> Oligonucleotide

<400> 193  
 cgagaggcac cccatatttatt tg 22

<210> 194  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 194  
 ttctctgtct catagtagtc ctcccc 26

<210> 195  
 <211> 1363  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
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 ccaagcctgg ccaaaccctg tgtttgaagg agatgccctg actctgcgat gtcagggatg 180  
 gaagaataca ccactgtctc aggtgaagtt ctacagagat ggaaaattcc ttcattttctc 240  
 taaggaaaac cagactctgt ccatggggagc agcaacagtg cagagccgtg gccagtacag 300  
 ctgctctggg caggtgatgt atattccaca gacattcaca caaacttcag agactgccat 360  
 ggttcaagtc caagagctgt ttccacctcc tgtgctgagt gccatccccct ctctgagcc 420  
 ccgagagggg agcctggtga ccctgagatg tcagacaaag ctgcaccccc tgaggtcagc 480  
 cttgaggctc cttttctcct tccacaagga cggccacacc ttgcaggaca ggggccctca 540  
 cccagaactc tgcattcccgg gagccaagga gggagactct gggctttact ggtgtgaggt 600

ggccccctgag ggtggccagg tccagaagca gagccccag ctggagggtca gagtgcaggc 660  
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 catggtgcag ctccctctgtg aggacacagag gggctcccct ccgatacctgt attccttcta 780  
 ccttgatgag aagattgtgg ggaaccactc agctccctgt ggtggaacca cctccctcct 840  
 cttcccagtg aagtcagaac aggatgctgg gaactactcc tgcgaggctg agaacagtgt 900  
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 gataccaccc acagctccag gtggagagca gtgccacta tatgccaacg tgcataccca 1140  
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 caccctggat ctccacacca agcggctcag ggttaatggt cgagttcagg aagcttatgt 1320  
 ggccttggtc aacacctgct cctcacccc cagcctgaag tga 1363

<210> 196  
 <211> 450  
 <212> PRT  
 <213> Homo sapiens

<400> 196

Met Leu Leu Trp Thr Ala Val Leu Leu Phe Gly Lys Ser Thr Ser Met  
1 5 10 15

Gly Ile Pro Ser Trp Ser Thr Lys Asp Leu Pro Cys Val Gly Lys Thr  
20 25 30

Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu Gly Asp  
35 40 45

Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu Ser Gln  
50 55 60

Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser Lys Glu Asn  
65 70 75 80

Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg Gly Gln Tyr  
85 90 95

Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe Thr Gln Thr  
100 105 110

Ser Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro Pro Pro Val  
115 120 125

Leu Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu Val Thr  
130 135 140

Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala Leu Arg Leu  
145 150 155 160

Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp Arg Gly Pro  
165 170 175

His Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser Gly Leu  
180 185 190

Tyr Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln Lys Gln Ser  
195 200 205

Pro Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg Pro Val Leu  
210 215 220

Thr Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp Met Val Gln  
225 230 235 240

Leu Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr Ser Phe  
245 250 255

Tyr Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro Cys Gly Gly  
260 265 270

Thr Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp Ala Gly Asn  
275 280 285

Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg Ser Glu Pro  
290 295 300

Lys Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr Pro Ala Ser  
305 310 315 320

Asn Trp Leu Val Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu Met Val  
325 330 335

Ile Ala Ala Ala Leu Leu Val Tyr Val Arg Ser Trp Arg Lys Ala Gly  
340 345 350

Pro Leu Pro Ser Gln Ile Pro Pro Thr Ala Pro Gly Gly Glu Gln Cys  
 355 360 365

Pro Leu Tyr Ala Asn Val His His Gln Lys Gly Lys Asp Glu Gly Val  
 370 375 380

Val Tyr Ser Val Val His Arg Thr Ser Lys Arg Ser Glu Ala Arg Ser  
 385 390 395 400

Ala Glu Phe Thr Val Gly Arg Lys His Lys Ala Ser Pro Lys Phe His  
 405 410 415

Pro Thr Leu Asp Leu His Thr Lys Arg Leu Arg Val Asn Gly Arg Val  
 420 425 430

Gln Glu Ala Tyr Val Ala Leu Val Asn Thr Cys Ser Leu Thr Pro Ser  
 435 440 445

Leu Lys  
 450

<210> 197  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 197  
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<210> 198  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 198  
 acaggaggtg gaaacagc 18

<210> 199  
 <211> 534  
 <212> DNA  
 <213> Homo sapiens

<400> 199

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 gacgtaggat gtgtacatgg ctctccaggt cagagttgct ccaagcaagg ttgttttgca 120  
 gaagtttctt ctatgtgtca ttcttttcta cactgtgtac tatgtgtccc tgagcatggg 180  
 ctgcgtgatg tttgaggtgc atgagttgaa tgtcctggct ccatttgatt tcaaaacaaa 240  
 tccctcatgg ctcaacataa actataaagt tcttttagtt tcaacagagg tcacctactt 300  
 tgtttgtgga ttgttttttg ttccagttgt ggaagaatgg gtttgggatt atgctatttc 360  
 agtcactatt cttcatgttg ccatcacttc aactgttatg ttggaattcc ccttgacatc 420  
 acattgggtg gctgcttttag gtatatcaaa attgcttggt tagattctct aatgcacaga 480  
 aataatgtta aatagaataa ctgtggaaat atattttatt ttctcataga tttt 534

<210> 200  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 200

Met Ala Leu Gln Val Arg Val Ala Pro Ser Lys Val Val Leu Gln Lys  
1 5 10 15

Phe Leu Leu Cys Val Ile Leu Phe Tyr Thr Val Tyr Tyr Val Ser Leu  
20 25 30

Ser Met Gly Cys Val Met Phe Glu Val His Glu Leu Asn Val Leu Ala  
35 40 45

Pro Phe Asp Phe Lys Thr Asn Pro Ser Trp Leu Asn Ile Asn Tyr Lys  
50 55 60

Val Leu Leu Val Ser Thr Glu Val Thr Tyr Phe Val Cys Gly Leu Phe  
65 70 75 80

Phe Val Pro Val Val Glu Glu Trp Val Trp Asp Tyr Ala Ile Ser Val  
85 90 95

Thr Ile Leu His Val Ala Ile Thr Ser Thr Val Met Leu Glu Phe Pro  
100 105 110

Leu Thr Ser His Trp Trp Ala Ala Leu Gly Ile Ser Lys Leu Leu Val  
115 120 125

<210> 201  
 <211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 201  
tcaaacaatca cgcagcccat 20

<210> 202  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 202  
tggggcctttc atcacctcct tg 22

<210> 203  
<211> 615  
<212> DNA  
<213> Homo sapiens

<400> 203  
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atattattttc tcttggttac ctcccgtcac atctctgtgg gcatttttgg agtactgtgc 180  
cttatgattg gtgagacagt tgaccgagaa ctacagaaag ctggctatga caatgccccat 240  
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aggatatgtg acaaaagttg ctatgcaatt atgggttgga gcactgtaac ctttatagct 360  
ggagttttatc agtgattggt ttgttaaatgt ggaagcaaca ttttctatga ttaaatctgct 420  
gttacctgtt ttgactgagc tactacaaaa agaaaaatca ctgaattgct atggggtttct 480  
gaaatatcca aaaaattaac ctgaagcagg gggaaaaatg acatcacacc attagcaggt 540  
attgtgtgaa acttctaaaa atgaaactga catttatctg acttattagg aataaatact 600  
ctctaatagaa ctctc 615

<210> 204  
<211> 121  
<212> PRT  
<213> Homo sapiens

<400> 204

Met Ser Gly Leu Ile Val Gly Ile Leu Leu Val Pro Gln Ser Ile Ala  
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Tyr Ser Leu Leu Ala Gly Gln Glu Pro Val Tyr Gly Leu Tyr Thr Ser  
20 25 30

Phe Phe Ala Ser Ile Ile Tyr Phe Leu Leu Gly Thr Ser Arg His Ile  
35 40 45

Ser Val Gly Ile Phe Gly Val Leu Cys Leu Met Ile Gly Glu Thr Val  
50 55 60

Asp Arg Glu Leu Gln Lys Ala Gly Tyr Asp Asn Ala His Ser Ala Pro  
65 70 75 80

Ser Leu Gly Met Val Ser Asn Gly Ser Thr Leu Leu Asn His Thr Ser  
85 90 95

Asp Arg Ile Cys Asp Lys Ser Cys Tyr Ala Ile Met Val Gly Ser Thr  
100 105 110

Val Thr Phe Ile Ala Gly Val Tyr Gln  
115 120

<210> 205  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 205  
taaatcatatc atcagacagg 20

<210> 206  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 206  
aaaacaggta acagcagatt 20

<210> 207  
<211> 513  
<212> DNA  
<213> Homo sapiens

<400> 207

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atggcgggcg cgcgtctcgc gagaattcgg cccgtcgggc tccaagcccg gcgcctggcg      60
tcggagggaa agactcgagc cgaaagcccc atctctgacc ctagcaactc ataccttct      120
ggcttccctt tagcaaagcg cctggacgtc atcccccttt cagatacccc aggcctcgtc      180
ctggccactg gcttgactat tgcaggagag cctgataaga tgggacacgg ctccaccttg      240
cattcagcaa gtcgttatcc tgcaactacg atgcaccagg aagaggatgt ggtgaggcca      300
gcttttccat atgcagttag gcatcgaagg gaagatctgc tgtacctaag tgggggtgggc      360
atttcatttt tagggaccgt ctttgttaaa ataatttggg acctcataaa gcctccagcc      420
attcctgatac aggcataagc ttacaacagc agcctgggtgc ccataacctg gacagcctgg      480
agtgaagtca cactcccaga cttgatgttc taa                                     513

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<210> 208
<211> 170
<212> PRT
<213> Homo sapiens

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<400> 208

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Met Ala Ala Ala Leu Ala Arg Ile Arg Pro Val Gly Leu Gln Ala
1          5          10          15

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Arg Arg Leu Ala Ser Glu Gly Lys Thr Arg Ala Glu Ser Pro Ile Ser
20          25          30

```

```

Asp Pro Ser Asn Ser Tyr Pro Ser Gly Phe Pro Leu Ala Lys Arg Leu
35          40          45

```

```

Asp Val Ile Pro Ser Ser Asp Thr Pro Gly Leu Val Leu Ala Thr Gly
50          55          60

```

```

Leu Thr Ile Ala Gly Glu Pro Asp Lys Met Gly His Gly Ser Thr Leu
65          70          75          80

```

```

His Ser Ala Ser Arg Tyr Pro Ala Thr Thr Met His Gln Glu Glu Asp
85          90          95

```

```

Val Val Arg Pro Ala Phe Pro Tyr Ala Val Arg His Arg Arg Glu Asp
100         105         110

```

```

Leu Leu Tyr Leu Ser Gly Val Gly Ile Ser Phe Leu Gly Thr Val Phe
115         120         125

```

```

Val Lys Ile Ile Trp Asp Leu Ile Lys Pro Pro Ala Ile Pro Asp Gln
130         135         140

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Asp Ile Ala Tyr Asn Ser Ser Leu Val Pro Ile Thr Trp Thr Ala Trp  
 145 150 155 160

Ser Glu Val Thr Leu Pro Asp Leu Met Phe  
 165 170

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 209  
 tgagccctag atatacttgg 20

<210> 210  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 210  
 cagtcagcct ccatttct 18

<210> 211  
 <211> 508  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
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 aatggaggct gactgaagga agagcagatt cacatctttc atcccttctt tatgctcatg 180  
 cttctaattt ttgttcccat gttttcttgc cctctctctt cttagcattt attttgtctg 240  
 tttctctttc cctctctctg gctccctctc catctctcct gagcacagaa atgcggtac 300  
 tgtatttaat ccacagtggc cccctctggc cccctctttg tgtctcctga gcacaggccc 360  
 tggccccctc tccatctctc ctgacctcct gatccgcca cctcgccag ttattgctgt 420  
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 gggaaggaag tagggaggca gggaagag 508

<210> 212

<211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 212

Met Pro Tyr Met Leu Glu Ser Pro Ser Val Cys Gln Ser Val His Thr  
 1 5 10 15

Val Arg Gly Ser Gln Lys Trp Arg Leu Thr Glu Gly Arg Ala Asp Ser  
 20 25 30

His Leu Ser Ser Leu Leu Tyr Ala His Ala Ser Asn Phe Cys Ser His  
 35 40 45

Val Phe Leu Pro Leu Leu Phe Leu Ala Phe Ile Leu Ser Val Ser Leu  
 50 55 60

Ser Pro Leu Leu Ala Pro Ser Pro Ser Leu Leu Ser Thr Glu Met Arg  
 65 70 75 80

Leu Leu Tyr Leu Ile His Ser Gly Pro Leu Trp Pro Pro Leu Cys Val  
 85 90 95

Ser

<210> 213  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 213  
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25

<210> 214  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 214  
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27

<210> 215  
 <211> 1321

<212> DNA  
 <213> Homo sapiens

<400> 215  
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 tgcaggcacc cgtgggaagc tccattcttg tgcagtgcc ctacaggctc caggatgtca 180  
 aagctcagaa ggtgtggtgc cggttcttgc cggaggggtg ccagcccctg gtgtcctcag 240  
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 aggaagaaga agagacccat aagattggca gtctggctga gaacgcattc tcagaccctg 480  
 caggcagtgc caaccctttg gaaccagcc aggatgagaa gagcatcccc ttgatctggg 540  
 gtgctgtgct cctggtaggt ctgctggtgg cagcgggtgg gctgtttgct gtgatggcca 600  
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 ccagcctacc tcttgattcc ccatcaggaa aaccttcact ccagctcca tcctcattgc 840  
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<210> 216  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 216

Met Gly Leu Thr Leu Leu Leu Leu Leu Leu Gly Leu Glu Gly Gln  
 1 5 10 15

Gly Ile Val Gly Ser Leu Pro Glu Val Leu Gln Ala Pro Val Gly Ser  
 20 25 30  
 Ser Ile Leu Val Gln Cys His Tyr Arg Leu Gln Asp Val Lys Ala Gln  
 35 40 45  
 Lys Val Trp Cys Arg Phe Leu Pro Glu Gly Cys Gln Pro Leu Val Ser  
 50 55 60  
 Ser Ala Val Asp Arg Arg Ala Pro Ala Gly Arg Arg Thr Phe Leu Thr  
 65 70 75 80  
 Asp Leu Gly Gly Gly Leu Leu Gln Val Glu Met Val Thr Leu Gln Glu  
 85 90 95  
 Glu Asp Ala Gly Glu Tyr Gly Cys Met Val Asp Gly Ala Arg Gly Pro  
 100 105 110  
 Gln Ile Leu His Arg Val Ser Leu Asn Ile Leu Pro Pro Glu Glu Glu  
 115 120 125  
 Glu Glu Thr His Lys Ile Gly Ser Leu Ala Glu Asn Ala Phe Ser Asp  
 130 135 140  
 Pro Ala Gly Ser Ala Asn Pro Leu Glu Pro Ser Gln Asp Glu Lys Ser  
 145 150 155 160  
 Ile Pro Leu Ile Trp Gly Ala Val Leu Leu Val Gly Leu Leu Val Ala  
 165 170 175  
 Ala Val Val Leu Phe Ala Val Met Ala Lys Arg Lys Gln Gly Asn Arg  
 180 185 190  
 Leu Gly Val Cys Gly Arg Phe Leu Ser Ser Arg Val Ser Gly Met Asn  
 195 200 205  
 Pro Ser Ser Val Val His His Val Ser Asp Ser Gly Pro Ala Ala Glu  
 210 215 220  
 Leu Pro Leu Asp Val Pro His Ile Arg Leu Asp Ser Pro Pro Ser Phe  
 225 230 235 240  
 Asp Asn Thr Thr Tyr Thr Ser Leu Pro Leu Asp Ser Pro Ser Gly Lys  
 245 250 255

Pro Ser Leu Pro Ala Pro Ser Ser Leu Pro Pro Leu Pro Pro Lys Val  
 260 265 270

Leu Val Cys Ser Lys Pro Val Thr Tyr Ala Thr Val Ile Phe Pro Gly  
 275 280 285

Gly Asn Lys Gly Gly Gly Thr Ser Cys Gly Pro Ala Gln Asn Pro Pro  
 290 295 300

Asn Asn Gln Thr Pro Ser Ser  
 305 310

<210> 217  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 217  
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<210> 218  
 <211> 18  
 <212> DNA  
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<220>  
 <223> Oligonucleotide

<400> 218  
 catcacagca aacagcac 18

<210> 219  
 <211> 3874  
 <212> DNA  
 <213> Homo sapiens

<400> 219  
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<210> 220

<211> 501  
 <212> PRT  
 <213> Homo sapiens

<400> 220

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Ala Gln Arg Thr Pro Gly Pro Glu Leu Arg Leu Ser Ser Gln Leu Leu  
 20 25 30

Pro Glu Leu Cys Thr Phe Val Val Arg Val Leu Phe Tyr Leu Gly Pro  
 35 40 45

Val Tyr Leu Ala Gly Tyr Leu Gly Leu Ser Ile Thr Trp Leu Leu Leu  
 50 55 60

Gly Ala Leu Leu Trp Met Trp Trp Arg Arg Asn Arg Arg Gly Lys Leu  
 65 70 75 80

Gly Arg Leu Ala Ala Ala Phe Glu Phe Leu Asp Asn Glu Arg Glu Phe  
 85 90 95

Ile Ser Arg Glu Leu Arg Gly Gln His Leu Pro Ala Trp Ile His Phe  
 100 105 110

Pro Asp Val Glu Arg Val Glu Trp Ala Asn Lys Ile Ile Ser Gln Thr  
 115 120 125

Trp Pro Tyr Leu Ser Met Ile Met Glu Ser Lys Phe Arg Glu Lys Leu  
 130 135 140

Glu Pro Lys Ile Arg Glu Lys Ser Ile His Leu Arg Thr Phe Thr Phe  
 145 150 155 160

Thr Lys Leu Tyr Phe Gly Gln Lys Cys Pro Arg Val Asn Gly Val Lys  
 165 170 175

Ala His Thr Asn Thr Cys Asn Arg Arg Arg Val Thr Val Asp Leu Gln  
 180 185 190

Ile Cys Tyr Ile Gly Asp Cys Glu Ile Ser Val Glu Leu Gln Lys Ile  
 195 200 205

Gln Ala Gly Val Asn Gly Ile Gln Leu Gln Gly Thr Leu Arg Val Ile  
 210 215 220



Leu Glu Pro Leu Leu Val Asp Lys Pro Phe Val Gly Ala Val Thr Val  
 225 230 235 240

Phe Phe Leu Gln Lys Gln His Leu Gln Ile Asn Trp Thr Gly Leu Thr  
 245 250 255

Asn Leu Leu Asp Ala Pro Gly Ile Asn Asp Val Ser Asp Ser Leu Leu  
 260 265 270

Glu Asp Leu Ile Ala Thr His Leu Val Leu Pro Asn Arg Val Thr Val  
 275 280 285

Pro Val Lys Lys Gly Leu Asp Leu Thr Asn Leu Arg Phe Pro Leu Pro  
 290 295 300

Cys Gly Val Ile Arg Val His Leu Leu Glu Ala Glu Gln Leu Ala Gln  
 305 310 315 320

Lys Asp Asn Phe Leu Gly Leu Arg Gly Lys Ser Asp Pro Tyr Ala Lys  
 325 330 335

Val Ser Ile Gly Leu Gln His Phe Arg Ser Arg Thr Ile Tyr Arg Asn  
 340 345 350

Leu Asn Pro Thr Trp Asn Glu Val Phe Glu Phe Met Val Tyr Glu Val  
 355 360 365

Pro Gly Gln Asp Leu Glu Val Asp Leu Tyr Asp Glu Asp Thr Asp Arg  
 370 375 380

Asp Asp Phe Leu Gly Ser Leu Gln Ile Cys Leu Gly Asp Val Met Thr  
 385 390 395 400

Asn Arg Val Val Asp Glu Trp Phe Val Leu Asn Asp Thr Thr Ser Gly  
 405 410 415

Arg Leu His Leu Arg Leu Glu Trp Leu Ser Leu Leu Thr Asp Gln Glu  
 420 425 430

Val Leu Thr Glu Asp His Gly Gly Leu Ser Thr Ala Ile Leu Val Val  
 435 440 445

Phe Leu Glu Ser Ala Cys Asn Leu Pro Arg Asn Pro Phe Asp Tyr Leu  
 450 455 460

Asn Gly Glu Tyr Arg Ala Lys Lys Leu Ser Arg Phe Ala Arg Val Lys  
 465 470 475 480

Gln Gly Gln Gln Arg Pro Phe Phe Leu Cys Gln Thr Ile Cys Arg Gln  
 485 490 495

Glu Asp Thr Tyr Lys  
 500

<210> 221  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 221  
 tggggcctgt ctacctagct 20

<210> 222  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 222  
 tcttggtggc ccactcgac 19

<210> 223  
 <211> 1020  
 <212> DNA  
 <213> Homo sapiens

<400> 223  
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 tccttaaaaa gtagcacttt gaagcctact attgaagcat tgcctaattgt gctaccttta 180  
 aatgaagatg ttaataagca ggaagaaaag aatgaagatc atactcccaa ttatgctcct 240  
 gctaattgaga aaaatggcaa ttattataaa gatataaaac aatatgtgtt cacaacacaa 300  
 aatccaaatg gcactgagtc tgaaatatct gtgagagcca caactgacct gaattttgct 360  
 ctaaaaaacg ataaaactgt caatgcaact acatatgaaa aatccaccat tgaagaagaa 420  
 acaactacta gcgaaccctc tcataaaaat attcaaagat caaccccaaa cgtgcctgca 480

ttttggacaa tgtagctaa agctataaat ggaacagcag tggatcatgga tgataaagat 540  
 caattatttc acccaattcc agagtctgat gtgaatgcta cacagggaga aaatcagcca 600  
 gatctagagg atctgaagat caaaataatg ctgggaatct cgttgatgac cctcctcctc 660  
 tttgtggtcc tcttggcatt ctgtagtgct aactgtaca aactgaggca tctgagttat 720  
 aaaagttgtg agagtcaagta ctctgtcaac ccagagctgg ccacgatgtc ttactttcat 780  
 ccatcagaag gtgtttcaga tacatccttt tccaagagtg cagagagcag cacatttttg 840  
 ggtaccactt cttcagatat gagaagatca ggcacaagaa catcagaatc taagataatg 900  
 acggatatca tttccatagg ctcagataat gagatgcatg aaaacgatga gtcggttacc 960  
 cgggtgaagaa atcaaggaac ccggtgaaga aatcttattg atgaataaat aactttaatt 1020

<210> 224  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 224

Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys  
 1 5 10 15

Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro  
 20 25 30

Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr  
 35 40 45

Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp  
 50 55 60

Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser  
 65 70 75 80

Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn  
 85 90 95

Asp Lys Thr Val Asn Ala Thr Thr Tyr Glu Lys Ser Thr Ile Glu Glu  
 100 105 110

Glu Thr Thr Thr Ser Glu Pro Ser His Lys Asn Ile Gln Arg Ser Thr  
 115 120 125

Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala Ile Asn Gly  
 130 135 140

Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His Pro Ile Pro  
 145 150 155 160

Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro Asp Leu Glu  
 165 170 175

Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met Thr Leu Leu  
 180 185 190

Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu Tyr Lys Leu  
 195 200 205

Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser Val Asn Pro  
 210 215 220

Glu Leu Ala Thr Met Ser Tyr Phe His Pro Ser Glu Gly Val Ser Asp  
 225 230 235 240

Thr Ser Phe Ser Lys Ser Ala Glu Ser Ser Thr Phe Leu Gly Thr Thr  
 245 250 255

Ser Ser Asp Met Arg Arg Ser Gly Thr Arg Thr Ser Glu Ser Lys Ile  
 260 265 270

Met Thr Asp Ile Ile Ser Ile Gly Ser Asp Asn Glu Met His Glu Asn  
 275 280 285

Asp Glu Ser Val Thr Arg  
 290

<210> 225  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 225  
 tgaatgctac acagggagaa aatc

24

<210> 226  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 226

tgaaagtaag acatcgtggc c

21

<210> 227

<211> 309

<212> DNA

<213> Homo sapiens

<400> 227

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ggagaagact tcctgtataa gagttctgga gccattgttg ctgccgttgt ggtgggtgtc 120

atcatcatct tcaccgtggt tctgatcctg ctgaagatgt acaacaggaa aatgaggacg 180

aggcggaac tagagcccaa gggccccaag ccaaccgcc cttctgccgt gggcccaaac 240

agcaacggca gccaacaccc agcaactgtg accttcagtc ctgttgacgt ccaggtggag 300

acgcgatga 309

<210> 228

<211> 102

<212> PRT

<213> Homo sapiens

<400> 228

Met Thr Thr Ala Thr Pro Leu Gly Asp Thr Thr Phe Phe Ser Leu Asn  
1 5 10 15

Met Thr Thr Arg Gly Glu Asp Phe Leu Tyr Lys Ser Ser Gly Ala Ile  
20 25 30

Val Ala Ala Val Val Val Val Val Ile Ile Ile Phe Thr Val Val Leu  
35 40 45

Ile Leu Leu Lys Met Tyr Asn Arg Lys Met Arg Thr Arg Arg Glu Leu  
50 55 60

Glu Pro Lys Gly Pro Lys Pro Thr Ala Pro Ser Ala Val Gly Pro Asn  
65 70 75 80

Ser Asn Gly Ser Gln His Pro Ala Thr Val Thr Phe Ser Pro Val Asp  
85 90 95

Val Gln Val Glu Thr Arg  
100

<210> 229  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 229  
 ggggatacca ccttcttct 19

<210> 230  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 230  
 agttgctggg tgttggt 18

<210> 231  
 <211> 2510  
 <212> DNA  
 <213> Homo sapiens

<400> 231  
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 gtcttctttt aagaagtgtc tgttcatatc ctttgccctt tcgcttctat gcaccaataa 180  
 caccagggt gagagtcaaa ccaagaacac aatcctgact acagtagcca taaagaaaat 240  
 gaaatacctg ggaatacacc taatcaaaaa catgaaagca ctctctagag ggagaactac 300  
 aaaacattgc tgaaagaaat cagagatgat tctctgaaaa agaagtcaga ttagaaatga 360  
 ttctctgaaa aagaaatcat ctctgatttc tttcagcagt gtgttttttg tttgtttgtt 420  
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<210> 232  
 <211> 164  
 <212> PRT  
 <213> Homo sapiens

<400> 232

Met Gln Arg Lys Arg Val Ser Ser Thr Lys Ser Leu Cys Trp Asp Gly  
1 5 10 15

Arg Phe Gly Pro Cys Gly Ala Ser Gly Lys Phe Trp Leu Gln Arg Lys  
20 25 30

Trp Arg Val Ser Gln Arg Arg Ser Lys Thr Lys Ser Gly Pro Val Leu  
35 40 45

Gly His Leu Lys Ala Met Pro Lys His Ser Val Ile Leu Gly Val His  
50 55 60

Trp Lys Ala Ser Ser Tyr Pro His Thr Ser Ser Gln Ser Pro Asp Val  
65 70 75 80

Asn Val Glu Ala Glu Asp His Leu Leu Leu Val Leu Leu Leu Phe Leu  
85 90 95

Leu Phe Leu Phe Arg Thr Ala Thr Ile Glu Asp Leu Ala Ser His Phe  
100 105 110

Pro Asp Val Phe Ser Glu Ile Leu Cys Trp Pro Ala Lys Pro Tyr Gly  
115 120 125

Phe Ile Leu Pro Leu Arg Ser Pro Ser Val Arg Ser Leu Phe Leu Lys  
130 135 140

Asp Arg Val Gly Ser Arg Arg Gly Thr Glu Arg Thr Ser Ser Leu Ala  
145 150 155 160

Leu Gln Cys Ser

<210> 233

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 233

gaggctgaga aaatggttaga

20

<210> 234

<211> 18



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 234  
tccatcccag caaagact 18

<210> 235  
<211> 1977  
<212> DNA  
<213> Homo sapiens

<400> 235  
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tcctgtgaga aacactcatt tgattgtgaa aagacttgaa ttctatgcta agcaggggttc 180  
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 aatatggaat tcacagatac acacacacat taaaaaatta acctagtgtg tctgtgagga 1620  
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 gtttatgtaa gtggaaaaag catgttgcaa aataacttgg tgtctatgat tcagtttatg 1800  
 taaaataata aatgtatgtg ggaatacgtg tgttgaaaga tgtacatcaa tttgctaaca 1860  
 atggttatct ctgacgtggg gggatttgag atgtgttttt ctttttggtt gtatttttct 1920  
 ctattgtttg acttaacaca gaacatgttt gggtacaaca ataaagttat tgaagac 1977

<210> 236  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 236

Met Ile Phe Pro Pro Ser Ser Arg Asp Gln Arg Glu Leu Ile Glu Cys  
 1 5 10 15

Asp Asn Asp Ser Leu Ala Gly Thr Ala Glu Ala Ser Gly Ser Phe Leu  
 20 25 30

Arg Ser Ala Val Lys Glu Asp Glu Lys His Gly Tyr Ala Leu Leu Leu  
 35 40 45

Val Pro Leu Phe Leu Tyr Leu Ile Ser Thr Ser Phe Tyr Lys Tyr Ile  
 50 55 60

Arg Ala Thr Leu Ser Leu Cys Ile Ser Asn Lys Ala Lys Arg Gly Cys  
 65 70 75 80

Asn Tyr Thr Leu Leu Gln Ser Ser Val Ser Pro Gly Asn Arg Asn Ala  
 85 90 95

Lys Ala Leu Lys Ala Ser Leu Phe Ala Asp Met Val Ser Trp Val Pro  
 100 105 110

Trp Ala Lys Ser Phe Cys Cys Pro Pro Leu Ser Pro Ser Lys Leu Gly  
 115 120 125

Pro Phe  
130

<210> 237  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 237  
atgattcttt agcagggga 18

<210> 238  
<211> 18  
<212> DNA  
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35 40 45

Phe Ala Lys Ile Phe Ile Gly Cys Leu Ala Ala Val Thr Ser Gly Met  
50 55 60

Met Tyr Ala Leu Tyr Leu Ser Ala Tyr His Glu Arg Lys Phe Trp Phe  
65 70 75 80

Ser Asn Arg Gln Glu Leu Glu Arg Glu Ile Thr Phe Gln Gly Asp Ser  
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Ala Ile Tyr Tyr Ser Tyr Tyr Lys Asp Met Leu Lys Ala Pro Ser Phe  
100 105 110

Glu Arg Gly Val Tyr Glu Leu Thr His Asn Asn Lys Thr Val Ser Leu  
115 120 125

Lys Thr Ile Asn Ala Val Gln Gln Met Ser Leu Tyr Pro Glu Leu Ile  
130 135 140

Ala Ser Ile Leu Tyr Gln Ala Thr Gly Ser Asn Glu Ile Ile Glu Pro  
145 150 155 160

Val Tyr Phe Tyr Ile Gly Ile Val Phe Gly Leu Gln Gly Ile Tyr Val  
165 170 175

Thr Ala Leu Phe Val Thr Ser Trp Leu Met Ser Gly Thr Trp Leu Ala  
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Gly Met Leu Thr Val Ala Trp Phe Val Ile Asn Ser Cys Thr Asp Pro  
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Cys Tyr Val Thr Tyr Leu Thr Phe Ser Ala Leu Ser Ser Lys Pro Ala  
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Glu Val Val Leu Asp Glu His Gly Lys Asn Val Thr Ile Cys Val Pro  
85 90 95

Asp Phe Gly Gln Asp Leu Tyr Arg Asp Glu Asn Leu Val Thr Ile Leu  
100 105 110

Gly Thr Ser Leu Leu Ile Gly Cys Ile Leu Tyr Ser Cys Leu Thr Ser  
115 120 125

Thr Thr Arg Ser Ser Ser Asp Ala Leu Gln Gly Arg Tyr Ala Ala Pro  
130 135 140

Glu Leu Glu Ile Ala Arg Cys Cys Phe Cys Phe Ser Pro Gly Gly Glu  
145 150 155 160

Asp Thr Glu Glu Gln Gln Pro Gly Lys Glu Gly Pro Arg Val Ile Tyr  
165 170 175

Asp Glu Lys Lys Gly Thr Val Tyr Ile Tyr Ser Tyr Phe His Phe Val  
180 185 190

Phe Phe Leu Ala Ser Leu Tyr Val Met Met Thr Val Thr Asn Trp Phe  
195 200 205

Asn Tyr Glu Ser Ala Asn Ile Glu Ser Phe Phe Ser Gly Ser Trp Ser  
210 215 220

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<213> Homo sapiens

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Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala Val Pro Cys  
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Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys Lys Glu Leu Gln  
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Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly Leu Ser Ser Pro Ala  
65 70 75 80

Gln Pro Pro Asp Pro Pro Arg Met Gly Glu Val Arg Ile Ala Ala Glu  
85 90 95

Glu Gly Arg Ala Val Val His Trp Cys Ala Pro Phe Ser Pro Val Leu  
100 105 110

His Tyr Trp Leu Leu Leu Trp Asp Gly Ser Glu Ala Ala Gln Lys Gly  
115 120 125

Pro Pro Leu Asn Ala Thr Val Arg Arg Ala Glu Leu Lys Gly Leu Lys  
130 135 140

Pro Gly Gly Ile Tyr Val Val Cys Val Val Ala Ala Asn Glu Ala Gly  
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Ala Ser Arg Val Pro Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp  
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Ile Pro Ala Phe Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro  
180 185 190

Arg Thr Leu Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu  
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Pro Ala Leu Pro Pro Arg Gly Leu Pro Cys Tyr Ser Ser Gly Gly Ala  
 35 40 45

Pro Ser Asn Ser Gly Pro Gln Gly His Gly Glu Ile His Arg Val Pro  
 50 55 60

Thr Gln Arg Arg Pro Ser Gln Phe Asp Lys Lys Ile Leu Leu Trp Thr  
 65 70 75 80

Gly Arg Phe Lys Ser Met Glu Glu Ile Pro Pro Arg Ile Pro Pro Glu  
 85 90 95

Met Ile Asp Thr Ala Arg Asn Lys Ala Arg Val Lys Ala Cys Tyr Ile  
 100 105 110

Met Ile Gly Leu Thr Ile Ile Ala Cys Phe Ala Val Ile Val Ser Ala  
 115 120 125

Lys Arg Ala Val Glu Arg His Glu Ser Leu Thr Ser Trp Asn Leu Ala  
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Lys Lys Ala Lys Trp Arg Glu Glu Ala Ala Leu Ala Ala Gln Ala Lys  
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Ala Ala Ala Val Ala Gly Trp Leu Val Val Ala Ser Met Ala Leu Leu  
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Gln Leu His Ala Val Gly Gly Val Ala Leu Thr Ser Ser His Pro Ser  
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Met Trp Ala Thr Gly Glu Glu Leu Arg Lys Pro Pro Trp Gln Gly Ser  
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ttgcagagtg	cactaaacag	ttgccccaga	aagacatgtc	ttgttttaaa	gcccagaacc	3180
tgaaattatt	atagatttta	ttcggtaata	aggaactttg	catgtgtaat	tacttaagga	3240
tatgaagatg	agatttgtct	ggattattaa	gcaccctaaa	tgccatgaca	ggtgtccttc	3300
caagagacag	aagaggagac	acagacacag	agcaggagga	cacgtggaga	cagaggcaga	3360
ctggagtgat	gcggccacaa	gcccagggac	acctggagcc	cccaggagct	gggagaggca	3420
ggaaggatcc	tcccctagag	cctccagggg	gaactggagg	atgcgtaaga	gaccagaac	3480
ttccacagaa	ggaggaaaat	taacctcctg	cttctctaga	ctgttccaaa	gctgaaccct	3540
agaaagcaaa	gctgatacag	aagcatccag	gctgcaggag	tacaggctgc	aagtgtgag	3600
cgtgggcctt	gggtgtgtct	catgggggaa	aaaaaactgt	gaaaaacctc	agagtagcat	3660



cttcacagta acgcacggac gatccctaaa ctgccttgta aacaaaaatg agagcttgag 3720  
tcagaggaag ccgagacaat atccttcttc gacaacgtgc gagaaccctg acgtcccca 3780  
gcaaaggaag acgttgcaag caggcaaaat gcgtcgattt ttttttttg tcagtatgat 3840  
gatttttgca gccacttggc tatggagagc agccgacacc ccctcttaca gccgtggatg 3900  
tttcttgaa gctgactcag tctgttcact ggttgagctt tgagtgaaaa gataacacag 3960  
gtctattgac tcacacacat gttttaagat ggaaaacttt acttctgttc ttggcaggac 4020  
atggagagag ggagggattc caaaaagtct cagcctccat caaggcgtgg cagctcatgc 4080  
cggtaatctc agcacttttg gaggtcagg cgggaggact gattgagtc gggtgttcaa 4140  
gggccaacct aggcaacaca gtgagaactc atctctgtaa aaaataaaaa taaaacatta 4200  
aaaaaaaaca tgagctttga agtgcacagg g 4231

<210> 260  
<211> 359  
<212> PRT  
<213> Homo sapiens

<400> 260

Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met  
1 5 10 15

Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu  
20 25 30

Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu  
35 40 45

Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn  
50 55 60

Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile  
65 70 75 80

Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys  
85 90 95

Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu  
100 105 110

Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro  
115 120 125

Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys  
 130 135 140

Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg  
 145 150 155 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe  
 165 170 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val  
 180 185 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile  
 195 200 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu  
 210 215 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala  
 225 230 235 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val  
 245 250 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr  
 260 265 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu  
 275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu  
 290 295 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr  
 305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu  
 325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu  
 340 345 350

Gln Arg Gln Glu Ser Val Phe  
 355

<210> 261  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 261  
 cctgttacct ggagaccct 19

<210> 262  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide

<400> 262  
 accagcgagt acaccacg 18

<210> 263  
 <211> 717  
 <212> DNA  
 <213> Homo sapiens

<400> 263  
 ggccgggctg gggcttcagc gggaggcagc agaggggaag tggtcagcgt ggcgaatgac 60  
 ggaagaaact cgcattgtct actggatcaa ggacagacag ctcaccaacc gtgacagcac 120  
 catactggaa cttcaaaaag ttctgaaaac atgttgtgct cagagcatga aaattttctg 180  
 ctgtcttttg aactttgtct acaaacagtt agaagatgca gccaaggggc tcaccatggg 240  
 tggcgatgtt gaagaacatg aagaccttac tgctgatagc accatcttca aatttgtgga 300  
 agcttataca gagtgggagg tgaagagggtg gtcagacaac aatctgataa tgaaacaaac 360  
 aaatgtgaag agaagacgct tagatgatgt tggccctgaa ttggaaaagg ctgtctggga 420  
 gctcggtgc ccaccagca ttcagtgtct gctacctcct gtctgttatg cttgtgtctg 480  
 gttttttcaa gttttaattt tttttttaat tcttagtttt tgtgggtaca tagtaggtgt 540  
 atatatttat gggttacatg agatgttttg atacaggcat gcaatatgta ataatacct 600  
 catggagaat ggggtaccca tcacatcaag catttatcct ttgtgttaca aacggtccag 660  
 ttagactctt ttagttatta ttaaaatgta caattaaatt atttttgact atagtca 717

<210> 264  
 <211> 171  
 <212> PRT  
 <213> Homo sapiens

<400> 264

Met Thr Glu Glu Thr Arg Ile Val Tyr Trp Ile Lys Asp Arg Gln Leu  
1 5 10 15

Thr Asn Arg Asp Ser Thr Ile Leu Glu Leu Gln Lys Val Leu Lys Thr  
20 25 30

Cys Cys Ala Gln Ser Met Lys Ile Phe Cys Cys Leu Trp Asn Phe Val  
35 40 45

Tyr Lys Gln Leu Glu Asp Ala Ala Gln Gly Leu Thr Met Gly Gly Asp  
50 55 60

Val Glu Glu His Glu Asp Leu Thr Ala Asp Ser Thr Ile Phe Lys Phe  
65 70 75 80

Val Glu Ala Tyr Thr Glu Trp Glu Val Lys Arg Trp Ser Asp Asn Asn  
85 90 95

Leu Ile Met Lys Gln Thr Asn Val Lys Arg Arg Arg Leu Asp Asp Val  
100 105 110

Gly Pro Glu Leu Glu Lys Ala Val Trp Glu Leu Gly Cys Pro Pro Ser  
115 120 125

Ile Gln Cys Leu Leu Pro Pro Val Cys Tyr Ala Cys Val Trp Phe Phe  
130 135 140

Gln Val Leu Ile Phe Phe Leu Ile Leu Ser Phe Cys Gly Tyr Ile Val  
145 150 155 160

Gly Val Tyr Ile Tyr Gly Leu His Glu Met Phe  
165 170

<210> 265

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 265

ttcaacatcg ccacccat

18

<210> 266

<211> 20

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 266  
cagcagaggg gaagtgggtca 20

<210> 267  
<211> 390  
<212> DNA  
<213> Homo sapiens

<400> 267  
atggaagtga tattaccaga caaacctcag gtagatgcac tggcctttct agctgctgtc 60  
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gatctggagg ttggagggtt agctggacag ccccttaaag ttttcaactcc acgtaaaaaa 180  
ggttctgggg aagtgggtga tgcttctcag tcgcccagca gaagcaatga tggccagcat 240  
tctgcattg gccacagcag agatctctgc tgctacactg ctcagaccct cataatctcc 300  
tacacatcaa atggtctttc tccttttagca actccaccct tccaccctat tcctggaaac 360  
tgctacgaca gtgttgatta taaaatatag 390

<210> 268  
<211> 129  
<212> PRT  
<213> Homo sapiens

<400> 268  
Met Glu Val Ile Leu Pro Asp Lys Pro Gln Val Asp Ala Leu Ala Phe  
1 5 10 15  
Leu Ala Ala Val Thr Met Leu Trp Ile Thr Leu Pro Met Ser Pro Phe  
20 25 30  
Ala Glu Ala Glu Lys Leu Ala Trp Asp Leu Glu Val Gly Gly Leu Ala  
35 40 45  
Gly Gln Pro Leu Lys Val Phe Thr Pro Arg Lys Lys Gly Ser Gly Glu  
50 55 60  
Val Gly Asp Ala Ser Gln Ser Pro Ser Arg Ser Asn Asp Gly Gln His  
65 70 75 80  
Ser Cys Ile Gly His Ser Arg Asp Leu Cys Cys Tyr Thr Ala Gln Thr  
85 90 95

Leu Ile Ile Ser Tyr Thr Ser Asn Gly Leu Ser Pro Leu Ala Thr Pro  
100 105 110

Pro Phe His Pro Ile Pro Gly Asn Cys Tyr Asp Ser Val Asp Tyr Lys  
115 120 125

Ile

<210> 269  
<211> 2856  
<212> DNA  
<213> Homo sapiens

<400> 269  
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cctgaactgg cagttccact cttcctagtg tttctcagtt tctatcttgt cacttttctg 120  
gggaatgggg ggatgatcat tctaatacaa gtggatgccc aactccacac ccccggtgac 180  
ttcttctga gccacctgc tttcctggat gcctgctgtg cctcagtaat caccctcag 240  
attctggcca cactggccac agacaagaca gttatctcct atggctgccg tgctgtgcag 300  
ttctctttct tcaccatatg tgcaggcaca gagtggtacc tgctgtcagt gatggcctat 360  
gaccgctttg ttgccattag caatccactg cactgtaaca tgaccatgac tccaggtagc 420  
tgcagggctt ttttggccag tgccttcac tgtgggggtg cagggggccat tctgcatacc 480  
acgtgcacct tcacctctc cttctgttgt gacaatcaga tcaacttctt cttctgtgac 540  
ctccccccc tgctgaagct cgctgcagc agcatgacac aaactgagat tgtcattctc 600  
ctttgtgcaa aatgcatgtt cctagccaat gtcattggtt tctgatctg ctacatgctc 660  
attatcagag ccattttgag ggtgaagtcg gcaggaggcc tctgatagc atctgctcat 720  
ttcgatgcat atgtatatga gacaggcatc aactacaaca cagtttatgg ctcaggaaag 780  
gcagtagggg ggtcctggag gagcctgcgg gaaaccaacc acatgagacc aggaaatact 840  
tcaaaacact cagcagccca gctgcatcaa tgcctcatcc agcaagttgg caggtggccc 900  
ttgcagagca tgcccttccc cgtttctgca gggccacctt ataagtcagt gcagcctctc 960  
cctggagacc cccggcctct cctgtgcac accggattat ttctgacttt gaagatgatg 1020  
gggtgtgggc ccaggaggcc cagggacagg aagtctgact tcttcataaa cacagaccct 1080  
gggtgcagggt caccagaaga acagaggtgt ggatgggaag ggcaccttc cactcctat 1140  
accctggggc tgtctctgcc agtcaacttc ggctgaaat gtccatgggtg gacactatct 1200

ggacccccag ctacctgcca acgtccagac ctgcagacac cttctccacc aaaggagata	1260
tgttcatccg ggctgcgacc ccttacacac agcgctggac cagacagaag tcaagttcca	1320
gcagcctccg gagcagccac tatgctgaca aaggggctgc ccgacatcac tgtgggactg	1380
cagatttatg actcctgcat ctcagggatc caggctctgg ggagcaccct ggccctgctg	1440
tccaatcagc ttccaccac aaccaactat gcttgtggct cccagcaaca tctcctgggc	1500
gtggttggag ggatgacctt cctggagtca gagcccatgt ctgagctgct ctccatctac	1560
agagtccctc agggccaaag actcaccaaa aactttgaag taaaagaact tgtctgcaca	1620
tatctggtag gacagcttcc ttatggcctg gtcagttatg acaacagcaa ctttgagtgg	1680
ctggatcagc agctgcagaa gcagatcggg ggcgaggac ttctgtttgg cgctgcgccc	1740
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tggctcggat taggggcttc catccaaagt gccagagaag gggcttggca tcgcacaggg	1860
ctggagaaca tgaccactgc ccacctgtct gccttcaaac ttctgatct aactgccact	1920
taccaagcct acctggcagc caaagccctg tgggttgccct atcagaactt gatgtcctgc	1980
tctgagagag agggaccatt cctgggaggc acgtatgcca atgcatggga agccaggctt	2040
tctcaggtta acttcaccac caaagcccaa gaagaggttt tcttcgcaa agatggggaa	2100
gtgctgacaa cgtttgacat taaaaacatc tatgttctcc cagacctgtc aggacagaca	2160
gccattgttg gacactttga cttcagagca cttcttgga aagagcttct gttggatgac	2220
agcgcaattg tctgggcaga aggaccctta aagattagag ctgagagAAC cctaagaacc	2280
aagaccacac agcacctctc acatcccaag ctccaggagt cccttcctct gtctgcaacg	2340
aaaaacgtcc tgtggaaacc aggaagtcaa ccctatttga gaagtcaaaa tgctgctaca	2400
aaagccttcc ctgaccaga agagaaatcg caatgtcacc agtttctctt tctcccttca	2460
gatagtgttg catgtcagaa gtgctctgac aaccagtggc ccaatgtgca gaagggcgag	2520
tgcatcccca aaacccttga cttcttggtc tatcacaagc cccttgacac agcgttggct	2580
gtctgcacag ccctgctctt tctccttgcc ctggccatct taggcatctt ccatgttgtc	2640
tgctcctgtg tctgggtgtc cttcatacct gccacatgc atgcccacag caaagacacc	2700
atggccatgg aggtctttgt catcttgga tcagcaggag gcctcatgtc ctccctcttc	2760
ttttccaaat gctacatcat ccttctccat cctgaaaaga acacaaaaga ccaaagtgtt	2820
ggccggcatc atcgcaagtg ggaaaaactg aagtga	2856

<210> 270

<211> 951

<212> PRT

<213> Homo sapiens

<400> 270

Met Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val  
1 5 10 15

Phe Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu  
20 25 30

Ser Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu  
35 40 45

Ile Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser  
50 55 60

His Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln  
65 70 75 80

Ile Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys  
85 90 95

Arg Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys  
100 105 110

Tyr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn  
115 120 125

Pro Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe  
130 135 140

Leu Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr  
145 150 155 160

Thr Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe  
165 170 175

Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met  
180 185 190

Thr Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu  
195 200 205

Ala Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala  
210 215 220



Ile Leu Arg Val Lys Ser Ala Gly Gly Leu Leu Ile Ala Ser Ala His  
 225 230 235 240  
 Phe Asp Ala Tyr Val Tyr Glu Thr Gly Ile Asn Tyr Asn Thr Val Tyr  
 245 250 255  
 Gly Ser Gly Lys Ala Val Gly Trp Ser Trp Arg Ser Leu Arg Glu Thr  
 260 265 270  
 Asn His Met Arg Pro Gly Asn Thr Ser Lys His Ser Ala Ala Gln Leu  
 275 280 285  
 His Gln Cys Leu Ile Gln Gln Val Gly Arg Trp Pro Leu Gln Ser Met  
 290 295 300  
 Pro Phe Pro Val Ser Ala Gly Pro Pro Tyr Lys Ser Val Gln Pro Leu  
 305 310 315 320  
 Pro Gly Asp Pro Arg Pro Leu Leu Cys Ile Thr Gly Leu Phe Leu Thr  
 325 330 335  
 Leu Lys Met Met Gly Cys Gly Pro Arg Arg Pro Arg Asp Arg Lys Ser  
 340 345 350  
 Asp Phe Phe Ile Asn Thr Asp Pro Gly Ala Gly Ser Pro Glu Glu Gln  
 355 360 365  
 Arg Cys Gly Trp Glu Gly His Pro Ser His Ser Tyr Thr Leu Gly Leu  
 370 375 380  
 Ser Leu Pro Val Asn Phe Gly Leu Lys Cys Pro Trp Trp Thr Leu Ser  
 385 390 395 400  
 Gly Pro Pro Ala Thr Cys Gln Arg Pro Asp Leu Gln Thr Pro Ser Pro  
 405 410 415  
 Pro Lys Glu Ile Cys Ser Ser Gly Leu Arg Pro Leu Thr His Ser Ala  
 420 425 430  
 Gly Pro Asp Arg Ser Gln Val Pro Ala Ala Ser Gly Ala Ala Thr Met  
 435 440 445  
 Leu Thr Lys Gly Leu Pro Asp Ile Thr Val Gly Leu Gln Ile Tyr Asp  
 450 455 460

Ser Cys Ile Ser Gly Ile Gln Ala Leu Gly Ser Thr Leu Ala Leu Leu  
 465 470 475 480

Ser Asn Gln Leu Pro Pro Thr Thr Asn Tyr Ala Cys Gly Ser Gln Gln  
 485 490 495

His Leu Leu Gly Val Val Gly Gly Met Thr Phe Leu Glu Ser Glu Pro  
 500 505 510

Met Ser Glu Leu Leu Ser Ile Tyr Arg Val Pro Gln Gly Gln Arg Leu  
 515 520 525

Thr Lys Asn Phe Glu Val Lys Glu Leu Val Cys Thr Tyr Leu Val Gly  
 530 535 540

Gln Leu Pro Tyr Gly Leu Val Ser Tyr Asp Asn Ser Asn Phe Glu Trp  
 545 550 555 560

Leu Asp Gln Gln Leu Gln Lys Gln Ile Gly Gly Glu Gly Leu Pro Val  
 565 570 575

Gly Ala Ala Pro Ser Arg Val Ala Arg Gln Gln Ser Asp Glu Glu Ala  
 580 585 590

Val Gly Gly Val Gln Gly Tyr Arg Trp Ser Gly Leu Gly Ala Ser Ile  
 595 600 605

Gln Ser Ala Arg Glu Gly Ala Trp His Arg Thr Gly Leu Glu Asn Met  
 610 615 620

Thr Thr Ala His Leu Ser Ala Phe Lys Leu Pro Asp Leu Thr Ala Thr  
 625 630 635 640

Tyr Gln Ala Tyr Leu Ala Ala Lys Ala Leu Trp Val Ala Tyr Gln Asn  
 645 650 655

Leu Met Ser Cys Ser Glu Arg Glu Gly Pro Phe Leu Gly Gly Thr Tyr  
 660 665 670

Ala Asn Ala Trp Glu Ala Arg Leu Ser Gln Val Asn Phe Thr Thr Lys  
 675 680 685

Ala Gln Glu Glu Val Phe Phe Ala Lys Asp Gly Glu Val Leu Thr Thr  
 690 695 700

Phe	Asp	Ile	Lys	Asn	Ile	Tyr	Val	Leu	Pro	Asp	Leu	Ser	Gly	Gln	Thr	705	710	715	720
Ala	Ile	Val	Gly	His	Phe	Asp	Phe	Arg	Ala	Pro	Ser	Gly	Lys	Glu	Leu	725	730	735	
Leu	Leu	Asp	Asp	Ser	Ala	Ile	Val	Trp	Ala	Glu	Gly	Pro	Leu	Lys	Ile	740	745	750	
Arg	Ala	Glu	Arg	Thr	Leu	Arg	Thr	Lys	Thr	Thr	Gln	His	Leu	Ser	His	755	760	765	
Pro	Lys	Leu	Gln	Glu	Ser	Leu	Pro	Leu	Ser	Ala	Thr	Lys	Asn	Val	Leu	770	775	780	
Trp	Lys	Pro	Gly	Ser	Gln	Pro	Tyr	Leu	Arg	Ser	Gln	Asn	Ala	Ala	Thr	785	790	795	800
Lys	Ala	Phe	Pro	Asp	Pro	Glu	Glu	Lys	Ser	Gln	Cys	His	Gln	Phe	Leu	805	810	815	
Phe	Leu	Pro	Ser	Asp	Ser	Val	Ala	Cys	Gln	Lys	Cys	Ser	Asp	Asn	Gln	820	825	830	
Trp	Pro	Asn	Val	Gln	Lys	Gly	Glu	Cys	Ile	Pro	Lys	Thr	Leu	Asp	Phe	835	840	845	
Leu	Phe	Tyr	His	Lys	Pro	Leu	Asp	Thr	Ala	Leu	Ala	Val	Cys	Thr	Ala	850	855	860	
Leu	Leu	Phe	Leu	Leu	Ala	Leu	Ala	Ile	Leu	Gly	Ile	Phe	His	Val	Val	865	870	875	880
Cys	Ser	Cys	Val	Trp	Val	Ser	Phe	Ile	Pro	Ala	His	Met	His	Ala	His	885	890	895	
Ser	Lys	Asp	Thr	Met	Ala	Met	Glu	Val	Phe	Val	Ile	Leu	Ala	Ser	Ala	900	905	910	
Gly	Gly	Leu	Met	Ser	Ser	Leu	Phe	Phe	Ser	Lys	Cys	Tyr	Ile	Ile	Leu	915	920	925	
Leu	His	Pro	Glu	Lys	Asn	Thr	Lys	Asp	Gln	Met	Phe	Gly	Arg	His	His	930	935	940	

Arg Lys Trp Glu Lys Leu Lys  
945 950

<210> 271  
<211> 956  
<212> DNA  
<213> Homo sapiens

<400> 271  
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ccacctggtg gcaatggctc agccacacct gacaatggca ccacccctgg ggccgagggc 120  
tggcggcagt tgctgggcct actccccgag cacatggcgg agaagctgtg tgaggcctgg 180  
gcctttgggc agagccacca gacgggcgtc gtggcactgg gcctactcac ctgcctgctg 240  
gcaatgctgc tggttggccg catcaggctc cggaggatcg atgccttctg cacctgcctg 300  
tgggccctgc tgctggggct gcacctggct gagcagcacc tgcaggccgc ctgccttagc 360  
tggctagaca cgctcaagtt cagcaccaca tctttgtgct gcctgggttg cttcacggcg 420  
gctgtggcca caaggaaggc aacgggcccc cggagggttc ggccccgaag gttcttccca 480  
ggagactctg ccggcctttt ccccaccagc ccagcttgg ccatccctca cccgagtgtc 540  
ggaggctctc cagcgtctct gttcatcccc agcccgcccc gcttctctgcc cctcgccaac 600  
caagcagctc ttccggtctc ctgcacggac ctacccctcc tcatttgcct ggccgcctca 660  
gccgggccct ctctctggga accataacct ctctgactcg agcagactcc ggctatctgt 720  
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ttacttctct cttcttctcg gggagctgc cctccgtcc catcctttcc cagggccttc 840  
cgggggcggc tcggtgggccc tccagtccgg ctctctggcc acgggaggcc ctcatcagcc 900  
tgccggtcaa cctgaggggac gaagtgtgtt gtccggcacc cctggagagg cccaaa 956

<210> 272  
<211> 231  
<212> PRT  
<213> Homo sapiens

<400> 272

Ala Ala Leu Tyr Gly Ala Ser Gly His Phe Ala Pro Gly Thr Thr Val  
1 5 10 15

Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly Ser Ala Thr Pro Asp Asn  
20 25 30

Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg Gln Leu Leu Gly Leu Leu  
35 40 45

Pro Glu His Met Ala Glu Lys Leu Cys Glu Ala Trp Ala Phe Gly Gln  
 50 55 60

Ser His Gln Thr Gly Val Val Ala Leu Gly Leu Leu Thr Cys Leu Leu  
 65 70 75 80

Ala Met Leu Leu Ala Gly Arg Ile Arg Leu Arg Arg Ile Asp Ala Phe  
 85 90 95

Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly Leu His Leu Ala Glu Gln  
 100 105 110

His Leu Gln Ala Ala Ser Pro Ser Trp Leu Asp Thr Leu Lys Phe Ser  
 115 120 125

Thr Thr Ser Leu Cys Cys Leu Val Gly Phe Thr Ala Ala Val Ala Thr  
 130 135 140

Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg Pro Arg Arg Phe Phe Pro  
 145 150 155 160

Gly Asp Ser Ala Gly Leu Phe Pro Thr Ser Pro Ser Leu Ala Ile Pro  
 165 170 175

His Pro Ser Val Gly Gly Ser Pro Ala Ser Leu Phe Ile Pro Ser Pro  
 180 185 190

Pro Ser Phe Leu Pro Leu Ala Asn Gln Ala Ala Leu Pro Val Ser Ser  
 195 200 205

Thr Asp Leu Thr Leu Leu Ile Cys Leu Ala Ala Ser Ala Gly Pro Ser  
 210 215 220

Leu Trp Glu Pro Tyr Pro Leu  
 225 230

<210> 273  
 <211> 1806  
 <212> DNA  
 <213> Homo sapiens

<400> 273  
 gaggaggcgc gcgtcgccgc cccgcgtccc gcctgcggcc cgcgcccccg gcgtcaccgc 60  
 ctctgcccc cctgccccgc tgcccgctg cccgcctacc cgcctaccgc cctaccgcgc 120

tacccccctg ccggcctgcc gtccttccac gcggagagcc atggagggag tgagcgcgct	180
gctggccccg tgccccacgg cggcctggc cggcggcctg ggggtcacgg cgtgcgccgc	240
ggccggcgtg ttgctctacc ggatcgcgcg gaggatgaag ccaacgcaca cgatgggtcaa	300
ctgctggttc tgcaaccagg atacgctggg gccctatggg aaccgcaact gctgggactg	360
tccccactgc gagcagtaca acggcttcca ggagaacggc gactacaaca agccgatccc	420
cgcccagtac ttggagcacc tgaaccacgt ggtgagcagc gcgccagcc tgcgcgaccc	480
ttcgcagccg cagcagtggg tgagcagcca agtcctgctg tgcaagaggt gcaaccacca	540
ccagaccacc aagatcaagc agctggccgc cttcgtcccc cgcgaggagg gcaggtatga	600
cgaggaggtc gaggtgtacc ggcacacact ggagcagatg tacaagctgt gccggccgtg	660
ccaagcggct gtggagtact acatcaagca ccagaaccgc cagctgcgcg ccctgttgtc	720
cagccaccag ttcaagcgcc gggaggccga ccagaccac gcacagaact tctcctccgc	780
cgtgaagtcc ccggtccagg tcatcctgct ccgtgccctc gccttcctgg cctgcgcctt	840
cctactgacc accgcgctgt atggggccag cggacacttc gcccaggca ccactgtgcc	900
cctggccctg ccacctggtg gcaatggctc agccacacct gacaatggca ccaccctgg	960
ggccgagggc tggcggcagt tgctgggcct actccccgag cacatggcgg agaagctgtg	1020
tgaggcctgg gcctttgggc agagccacca gacgggcgtc gtggcactgg gcctactcac	1080
ctgcctgctg gcaatgctgc tggtggccg catcaggctc cggaggatcg atgccttctg	1140
cacctgcctg tgggccctgc tgctggggct gcacctggct gagcagcacc tgcaggccgc	1200
ctcgcctagc tggctagaca cgtcaagtt cagcaccaca tctttgtgct gcctggttgg	1260
cttcacggcg gctgtggcca caaggaaggc aacgggcca cggaggttcc ggccccgaag	1320
gttcttccca ggagactctg ccggcctttt ccccaccagc ccagcttgg ccatccctca	1380
cccagtgctc ggaggctctc cagcgtctct gtcatcccc agcccggcca gcttctgccc	1440
cctcgccaac caagcagctc ttccggtctc ctcgacggac ctcaccctcc tcatttgcct	1500
ggccgcctca gccgggccct ctctctggga accataccct ctctgactcg agcagactcc	1560
ggctatctgt tcagcggtag ccgcccacca tctcagggtg ctcgatctgg gggagtttcc	1620
tgttttcaga ttacttctct cttcttgctg ggggaagctg ccctccgtcc catcctttcc	1680
cagggccttc cgggggcggc tcggtgggccc tccagtccgg ctctctggcc acgggaggcc	1740
ctcatcagcc tgccggtcaa cctgagggac gaagtgtgtt gtccggcacc cctggagagg	1800
cccaaa	1806

<211> 461  
 <212> PRT  
 <213> Homo sapiens

<400> 274

Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu  
 1 5 10 15

Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu  
 20 25 30

Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys  
 35 40 45

Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys  
 50 55 60

Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly  
 65 70 75 80

Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His  
 85 90 95

Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln  
 100 105 110

Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln  
 115 120 125

Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly  
 130 135 140

Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met  
 145 150 155 160

Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys  
 165 170 175

His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys  
 180 185 190

Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val  
 195 200 205

Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala  
 210 215 220

Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe  
 225 230 235 240

Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly  
 245 250 255

Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg  
 260 265 270

Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu  
 275 280 285

Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly  
 290 295 300

Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu  
 305 310 315 320

Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly  
 325 330 335

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu  
 340 345 350

Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe  
 355 360 365

Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg  
 370 375 380

Pro Arg Arg Phe Phe Pro Gly Asp Ser Ala Gly Leu Phe Pro Thr Ser  
 385 390 395 400

Pro Ser Leu Ala Ile Pro His Pro Ser Val Gly Gly Ser Pro Ala Ser  
 405 410 415

Leu Phe Ile Pro Ser Pro Pro Ser Phe Leu Pro Leu Ala Asn Gln Ala  
 420 425 430

Ala Leu Pro Val Ser Ser Thr Asp Leu Thr Leu Leu Ile Cys Leu Ala  
 435 440 445

Ala Ser Ala Gly Pro Ser Leu Trp Glu Pro Tyr Pro Leu  
 450 455 460



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<210> 275
<211> 600
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (460)..(460)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (530)..(530)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (574)..(574)
<223> n is a, c, g, t or u

<220>
<221> misc_feature
<222> (577)..(577)
<223> n is a, c, g, t or u

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<400> 275
tcaagtctga cttgcatcta cactgcgggc aagatgcggc tgcaagaccg catcgccacg      60
ttctttcttc caaaaggcat gatgctcacc acggtgcgc tgatgctctt cttcttacac      120
ctgggcatct tcatcagaga cgtgcacaac ttctgcatca cctaccacta tgaccacatg      180
agctttcact acacggtcgt cctgatgttc tcccaggtga tcagcatctg ctgggctgcc      240
atggggtcac tctatgctga gatgacagaa aacaagtacg tctgcttctc cgccctgacc      300
atcctgagtg agtggcagga gggggagggg gcaagaggga gcggggagct ttggaaccct      360
gagatgtggc aaggagtagc caggaagggt tactggggct catggggggc tctgtcccc      420
gccagtgct caacggagcc atgctcttca accgcctgtn cttggagttt ctggccatcg      480
agtaccggga ggagcaccac tgaggcctgg ggagtcggaa cagggctaan gagggggaag      540
caaaaggctg cctcgggtgt ttaataaag ctgntgntta tttccaaaaa aaaaaaaaaa      600

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<210> 276
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (128)..(128)
<223> Xaa is S, P, T or A

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<220>  
 <221> UNSURE  
 <222> (151)..(151)  
 <223> Xaa is M, T, K or R

<220>  
 <221> UNSURE  
 <222> (166)..(166)  
 <223> Xaa is L, M or V

<220>  
 <221> UNSURE  
 <222> (167)..(167)  
 <223> Xaa is F, L, I or V

<400> 276

Met Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly  
 1 5 10 15

Ile Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp  
 20 25 30

His Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile  
 35 40 45

Ser Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu  
 50 55 60

Asn Lys Tyr Val Cys Phe Ser Ala Leu Thr Ile Leu Ser Glu Trp Gln  
 65 70 75 80

Glu Gly Glu Gly Ala Arg Gly Ser Gly Glu Leu Trp Asn Pro Glu Met  
 85 90 95

Trp Gln Gly Val Ala Arg Glu Gly Tyr Trp Gly Ser Trp Gly Ala Leu  
 100 105 110

Ser Pro Ala Gln Cys Ser Thr Glu Pro Cys Ser Ser Thr Ala Cys Xaa  
 115 120 125

Trp Ser Phe Trp Pro Ser Ser Thr Gly Arg Ser Thr Thr Glu Ala Trp  
 130 135 140

Gly Val Gly Thr Gly Leu Xaa Arg Gly Lys Gln Lys Ala Ala Ser Gly  
 145 150 155 160

Val Leu Ile Lys Leu Xaa Xaa Ile Ser Lys Lys Lys Lys Lys  
 165 170

<210> 277  
 <211> 457  
 <212> DNA  
 <213> Homo sapiens

<400> 277  
 aaacactgca ggctacgaat cggtcattgc atagggttttc catgaatcag gaagattcag 60  
 tcctggtaaa ttcattccca ggaacatcgc tgccactgct attattctag cagctgttcc 120  
 catactccaa tgagtccagt taaacatttg ccttcttggg tcatgtaaag gtggcctgaa 180  
 gactgccaga agaggctgaa gaactgccaa agtcatcact atacagccga ggtatgggtg 240  
 gtaacctgca tgctactcc agcctccct gtatataaac ggcataacaa aagcaatgca 300  
 ggtgaggaca gttgtggtga acatgagcat cccgatgcacc tgaaaccaag ctgcttcacc 360  
 aagcaagaaa gcttttgacc aaactggctt gaagaaccgg gcaaccagta cacctatgct 420  
 aacagtagtc atccatgccaa caaacattaa ggcacca 457

<210> 278  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 278  
 Met Phe Val Ala Trp Met Thr Thr Val Ser Ile Gly Val Leu Val Ala  
 1 5 10 15  
 Arg Phe Phe Lys Pro Val Trp Ser Lys Ala Phe Leu Leu Gly Glu Ala  
 20 25 30  
 Ala Trp Phe Gln Val His Arg Met Leu Met Phe Thr Thr Thr Val Leu  
 35 40 45  
 Thr Cys Ile Ala Phe Val Met Pro Phe Ile Tyr Arg Gly Gly Trp Ser  
 50 55 60  
 Arg His Ala Gly Tyr His Pro Tyr Leu Gly Cys Ile Val Met Thr Leu  
 65 70 75 80  
 Ala Val Leu Gln Pro Leu Leu Ala Val Phe Arg Pro Pro Leu His Asp  
 85 90 95  
 Pro Arg Arg Gln Met Phe Asn Trp Thr His Trp Ser Met Gly Thr Ala  
 100 105 110  
 Ala Arg Ile Ile Ala Val Ala Ala Met Phe Leu Gly Met Asn Leu Pro

115

120

125

Gly Leu Asn Leu Pro Asp Ser Trp Lys Thr Tyr Ala Met Thr Asp Ser  
 130 135 140

<210> 279  
 <211> 293  
 <212> DNA  
 <213> Homo sapiens

<400> 279  
 tttttttttt tttttttaag gctgaagcaa ataggaacgt atattttctca tgaatccaaa 60  
 gcaaagacac aggaagtgtt ggcattcttt tgggtggtgg tagctcttga cttctcttctc 120  
 aagggttgcca catgccttag cagcagctca tgacttcacg ttctcaccgt attcgaagggc 180  
 aggaagcatg gagtagctgg cagctgcgtt tgacacagac tgccttcgga ccccttctcc 240  
 gcgcagtgcg actcgcaatt gtctggagca cgttggcagc agccctcgtg ccg 293

<210> 280  
 <211> 45  
 <212> PRT  
 <213> Homo sapiens

<400> 280  
 Arg His Glu Gly Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His  
 1 5 10 15

Cys Ala Glu Lys Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Leu Pro  
 20 25 30

Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val Arg Thr  
 35 40 45

<210> 281  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 281  
 Cys Gln Lys Gln Arg Asn Trp His Gly Ile Trp Arg Leu Glu Val  
 1 5 10 15

<210> 282  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 282

Met Ala Lys Gln Gly Glu Met Asn Thr Ser Thr Ser Cys  
1 5 10

<210> 283  
<211> 13  
<212> PRT  
<213> Homo sapiens  
  
<400> 283

Pro Lys Arg Gly Gly Arg Ala Gly Arg Glu His Ser Cys  
1 5 10

<210> 284  
<211> 91  
<212> PRT  
<213> Homo sapiens  
  
<400> 284

Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu  
1 5 10 15

Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp  
20 25 30

Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe  
35 40 45

Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met  
50 55 60

Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly  
65 70 75 80

Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr  
85 90

<210> 285  
<211> 15  
<212> PRT  
<213> Homo sapiens  
  
<400> 285

Cys Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser  
1 5 10 15

<210> 286  
<211> 14

<212> PRT  
<213> Homo sapiens

<400> 286

Cys Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr  
1 5 10

<210> 287  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 287

Met Ala Cys Ile Tyr Pro Thr Thr Phe Tyr Thr Ser Leu Pro Thr Lys  
1 5 10 15

Ser Leu Asn

<210> 288  
<211> 121  
<212> PRT  
<213> Homo sapiens

<400> 288

Ala Pro Pro Ser Cys Arg Glu Cys Tyr Gln Ser Leu His Tyr Arg Gly  
1 5 10 15

Glu Met Gln Gln Tyr Phe Thr Tyr His Thr His Ile Glu Arg Ser Cys  
20 25 30

Tyr Gly Asn Leu Ile Glu Glu Cys Val Glu Ser Gly Lys Ser Tyr Tyr  
35 40 45

Lys Val Lys Asn Leu Gly Val Cys Gly Ser Arg Asn Gly Ala Ile Cys  
50 55 60

Pro Arg Gly Lys Gln Trp Leu Cys Phe Thr Lys Ile Gly Gln Trp Gly  
65 70 75 80

Val Asn Thr Gln Val Leu Glu Asp Ile Lys Arg Glu Gln Ile Ile Ala  
85 90 95

Lys Ala Lys Ala Ser Lys Pro Thr Thr Pro Pro Glu Asn Arg Pro Arg  
100 105 110

His Phe His Ser Phe Ile Gln Lys Leu

115

120

<210> 289  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 289

Cys Glu Asn Arg Pro Arg His Phe His Ser Phe Ile Gln Lys Leu  
 1 5 10 15

<210> 290  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 290

Cys Ile Tyr Pro Thr Thr Phe Tyr Thr Ser Leu Pro Thr  
 1 5 10

<210> 291  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 291

Cys Lys Glu Asp Glu Leu Val Arg Asp Ser Pro Ala Arg Lys  
 1 5 10

<210> 292  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Ala Leu Gly Thr Arg Leu Ser Gln His Thr Asp Val  
 1 5 10

<210> 293  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 293

Asp Phe Asn Cys Pro Cys Leu Val His Tyr Asn  
 1 5 10

<210> 294  
 <211> 53

<212> PRT  
 <213> Homo sapiens  
  
 <400> 294  
 Ser Ser Ser Val Asp Pro Glu Lys Phe Leu Asp Phe Ala Asn Met Thr  
 1 5 10 15  
  
 Pro Ser Gln Val Gln Leu Phe Leu Ala Lys Val Pro Cys Lys Glu Asp  
 20 25 30  
  
 Glu Leu Val Arg Asp Ser Pro Ala Arg Lys Ala Val Ser Arg Tyr Leu  
 35 40 45  
  
 Arg Cys Leu Ser Gln  
 50  
  
 <210> 295  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 295  
 Arg Cys Leu Arg Pro Cys Phe Asp Gln Thr Val Phe Leu Gln Arg Arg  
 1 5 10 15  
  
 Tyr Trp Ser Asn Tyr Val Asp Leu Glu Gln Lys Leu Phe Asp Glu Thr  
 20 25 30  
  
 Cys Cys Glu His Ala Arg Asp Phe Ala His Arg Cys Val Leu His Phe  
 35 40 45  
  
 Phe Ala Ser Met Arg Ser Glu Leu Gln Ala Arg Gly Leu Arg Arg Gly  
 50 55 60  
  
 Asn Ala Gly Arg Arg Leu Glu Leu Pro Ala Val Pro Glu Pro Pro Glu  
 65 70 75 80  
  
 Gly Leu Asp Ser Gly Ser Gly Lys Ala His Leu Arg Ala Ile Ser Ser  
 85 90 95  
  
 Arg Glu Gln Val Asp Arg Leu Leu Ser Thr Trp Tyr Ser Ser Lys Pro  
 100 105 110  
  
 Pro Leu Asp Leu Ala Ala Ser Pro Gly Leu Cys Gly Gly Gly Leu Ser  
 115 120 125



His Arg Ala Pro Thr Leu Ala Leu Gly Thr Arg Leu Ser Gln His Thr  
 130 135 140

Asp Val  
 145

<210> 296  
 <211> 1035  
 <212> PRT  
 <213> Homo sapiens

<400> 296

Met Pro Cys Gly Phe Ser Pro Ser Pro Val Ala His His Leu Val Pro  
 1 5 10 15

Gly Pro Pro Asp Thr Pro Ala Gln Gln Leu Arg Cys Gly Trp Thr Val  
 20 25 30

Gly Gly Trp Leu Leu Ser Leu Val Arg Gly Leu Leu Pro Cys Leu Pro  
 35 40 45

Pro Gly Ala Arg Thr Ala Glu Gly Pro Ile Met Val Leu Ala Gly Pro  
 50 55 60

Leu Ala Val Ser Leu Leu Leu Pro Ser Leu Thr Leu Leu Val Ser His  
 65 70 75 80

Leu Ser Ser Ser Gln Asp Val Ser Ser Glu Pro Ser Ser Glu Gln Gln  
 85 90 95

Leu Cys Ala Leu Ser Lys His Pro Thr Val Ala Phe Glu Asp Leu Gln  
 100 105 110

Pro Trp Val Ser Asn Phe Thr Tyr Pro Gly Ala Arg Asp Phe Ser Gln  
 115 120 125

Leu Ala Leu Asp Pro Ser Gly Asn Gln Leu Ile Val Gly Ala Arg Asn  
 130 135 140

Tyr Leu Phe Arg Leu Ser Leu Ala Asn Val Ser Leu Leu Gln Ala Thr  
 145 150 155 160

Glu Trp Ala Ser Ser Glu Asp Thr Arg Arg Ser Cys Gln Ser Lys Gly  
 165 170 175

Lys Thr Glu Glu Glu Cys Gln Asn Tyr Val Arg Val Leu Ile Val Ala

180

185

190

Gly Arg Lys Val Phe Met Cys Gly Thr Asn Ala Phe Ser Pro Met Cys  
195 200 205

Thr Ser Arg Gln Val Gly Asn Leu Ser Arg Thr Ile Glu Lys Ile Asn  
210 215 220

Gly Val Ala Arg Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val  
225 230 235 240

Ile Ser Ser Gln Gly Glu Leu Tyr Ala Ala Thr Val Ile Asp Phe Ser  
245 250 255

Gly Arg Asp Pro Ala Ile Tyr Arg Ser Leu Gly Ser Gly Pro Pro Leu  
260 265 270

Arg Thr Ala Gln Tyr Asn Ser Lys Trp Leu Asn Glu Pro Asn Phe Val  
275 280 285

Ala Ala Tyr Asp Ile Gly Leu Phe Ala Tyr Phe Phe Leu Arg Glu Asn  
290 295 300

Ala Val Glu His Asp Cys Gly Arg Thr Val Tyr Ser Arg Val Ala Arg  
305 310 315 320

Val Cys Lys Asn Asp Val Gly Gly Arg Phe Leu Leu Glu Asp Thr Trp  
325 330 335

Thr Thr Phe Met Lys Ala Arg Leu Asn Cys Ser Arg Pro Gly Glu Val  
340 345 350

Pro Phe Tyr Tyr Asn Glu Leu Gln Ser Ala Phe His Leu Pro Glu Gln  
355 360 365

Asp Leu Ile Tyr Gly Val Phe Thr Thr Asn Val Asn Ser Ile Ala Ala  
370 375 380

Ser Ala Val Cys Ala Phe Asn Leu Ser Ala Ile Ser Gln Ala Phe Asn  
385 390 395 400

Gly Pro Phe Arg Tyr Gln Glu Asn Pro Arg Ala Ala Trp Leu Pro Ile  
405 410 415

Ala Asn Pro Ile Pro Asn Phe Gln Cys Gly Thr Leu Pro Glu Thr Gly

420

425

430

Pro Asn Glu Asn Leu Thr Glu Arg Ser Leu Gln Asp Ala Gln Arg Leu  
 435 440 445

Phe Leu Met Ser Glu Ala Val Gln Pro Val Thr Pro Glu Pro Cys Val  
 450 455 460

Thr Gln Asp Ser Val Arg Phe Ser His Leu Val Val Asp Leu Val Gln  
 465 470 475 480

Ala Lys Asp Thr Leu Tyr His Val Leu Tyr Ile Gly Thr Glu Ser Gly  
 485 490 495

Thr Ile Leu Lys Ala Leu Ser Thr Ala Ser Arg Ser Leu His Gly Cys  
 500 505 510

Tyr Leu Glu Glu Leu His Val Leu Pro Pro Gly Arg Arg Glu Pro Leu  
 515 520 525

Arg Ser Leu Arg Ile Leu His Ser Ala Arg Ala Leu Phe Val Gly Leu  
 530 535 540

Arg Asp Gly Val Leu Arg Val Pro Leu Glu Arg Cys Ala Ala Tyr Arg  
 545 550 555 560

Ser Gln Gly Ala Cys Leu Gly Ala Arg Asp Pro Tyr Cys Gly Trp Asp  
 565 570 575

Gly Lys Gln Gln Arg Cys Ser Thr Leu Glu Asp Ser Ser Asn Met Ser  
 580 585 590

Leu Trp Thr Gln Asn Ile Thr Ala Cys Pro Val Arg Asn Val Thr Arg  
 595 600 605

Asp Gly Gly Phe Gly Pro Trp Ser Pro Trp Gln Pro Cys Glu His Leu  
 610 615 620

Asp Gly Asp Asn Ser Gly Ser Cys Leu Cys Arg Ala Arg Ser Cys Asp  
 625 630 635 640

Ser Pro Arg Pro Arg Cys Gly Gly Leu Asp Cys Leu Gly Pro Ala Ile  
 645 650 655

His Ile Ala Asn Cys Ser Arg Asn Gly Ala Trp Thr Pro Trp Ser Ser

660	665	670
Trp Ala Leu Cys Ser Thr Ser Cys Gly Ile Gly Phe Gln Val Arg Gln		
675	680	685
Arg Ser Cys Ser Asn Pro Ala Pro Arg His Gly Gly Arg Ile Cys Val		
690	695	700
Gly Lys Ser Arg Glu Glu Arg Phe Cys Asn Glu Asn Thr Pro Cys Pro		
705	710	715 720
Val Pro Ile Phe Trp Ala Ser Trp Gly Ser Trp Ser Lys Cys Ser Ser		
	725	730 735
Asn Cys Gly Gly Gly Met Gln Ser Arg Arg Arg Ala Cys Glu Asn Gly		
	740	745 750
Asn Ser Cys Leu Gly Cys Gly Val Glu Phe Lys Thr Cys Asn Pro Glu		
	755	760 765
Gly Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr Pro Trp Leu Pro		
	770	775 780
Val Asn Val Thr Gln Gly Gly Ala Arg Gln Glu Gln Arg Phe Arg Phe		
785	790	795 800
Thr Cys Arg Ala Pro Leu Ala Asp Pro His Gly Leu Gln Phe Gly Arg		
	805	810 815
Arg Arg Thr Glu Thr Arg Thr Cys Pro Ala Asp Gly Ser Gly Ser Cys		
	820	825 830
Asp Thr Asp Ala Leu Val Glu Val Leu Leu Arg Ser Gly Ser Thr Ser		
	835	840 845
Pro His Thr Val Ser Gly Gly Trp Ala Ala Trp Gly Pro Trp Ser Ser		
	850	855 860
Cys Ser Arg Asp Cys Glu Leu Gly Phe Arg Val Arg Lys Arg Thr Cys		
865	870	875 880
Thr Asn Pro Glu Pro Arg Asn Gly Gly Leu Pro Cys Val Gly Asp Ala		
	885	890 895
Ala Glu Tyr Gln Asp Cys Asn Pro Gln Ala Cys Pro Val Arg Gly Ala		

900	905	910
Trp Ser Cys Trp Thr Ser Trp Ser Pro Cys Ser Ala Ser Cys Gly Gly		
915	920	925
Gly His Tyr Gln Arg Thr Arg Ser Cys Thr Ser Pro Ala Pro Ser Pro		
930	935	940
Gly Glu Asp Ile Cys Leu Gly Leu His Thr Glu Glu Ala Leu Cys Ala		
945	950	955 960
Thr Gln Ala Cys Pro Glu Gly Trp Ser Pro Trp Ser Glu Trp Ser Lys		
	965	970 975
Cys Thr Asp Asp Gly Ala Gln Ser Arg Ser Arg His Cys Glu Glu Leu		
	980	985 990
Leu Pro Gly Ser Ser Ala Cys Ala Gly Asn Ser Ser Gln Ser Arg Pro		
	995	1000 1005
Cys Pro Tyr Ser Glu Ile Pro Val Ile Leu Pro Ala Ser Ser Met		
	1010	1015 1020
Glu Glu Ala Thr Asp Cys Ala Gly Phe Asn Leu Ile		
	1025	1030 1035
<210> 297		
<211> 16		
<212> PRT		
<213> Homo sapiens		
<400> 297		
Cys Pro Tyr Asp Pro Arg His Asn Ser Thr Ala Val Ile Ser Ser Gln		
1	5	10 15
<210> 298		
<211> 11		
<212> PRT		
<213> Homo sapiens		
<400> 298		
Cys Pro Glu Val Arg Arg Asn Thr Pro Trp Thr		
1	5	10
<210> 299		
<211> 35		
<212> PRT		

<213> Homo sapiens

<400> 299

Glu Arg Val Trp Ser Asp Asp His Lys Asp Phe Asp Cys Asn Thr Arg  
1 5 10 15

Gln Pro Gly Cys Ser Asn Val Cys Phe Asp Glu Phe Phe Pro Val Ser  
20 25 30

His Val Arg  
35

<210> 300

<211> 38

<212> PRT

<213> Homo sapiens

<400> 300

His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro Val Val Lys Cys His  
1 5 10 15

Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe Ile Ser Lys Pro Ser  
20 25 30

Glu Lys Asn Ile Phe Thr  
35

<210> 301

<211> 15

<212> PRT

<213> Homo sapiens

<400> 301

Cys Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile Leu  
1 5 10 15

<210> 302

<211> 13

<212> PRT

<213> Homo sapiens

<400> 302

Glu Arg Val Trp Ser Asp Asp His Lys Asp Phe Asp Cys  
1 5 10

<210> 303

<211> 38

<212> PRT

<213> Homo sapiens

<400> 303

Asn Asn Asp Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly  
1 5 10 15

Ser Asn Gln Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser Asp  
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Asp Ser Ser Ser Arg Ile  
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Cys Val Pro His Ser Arg Ser Arg Gly Pro Asn Leu  
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Val Ser Gln Asp Gly Ala Asp Tyr Ser Val Gly Val Cys Val Pro Asp  
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Ser Cys Ala Glu Glu Asp Val Thr Leu Met Ser Arg Leu Asp Thr Leu  
 35 40 45

Arg Phe Arg Asn Thr Ser Phe Leu Ala Pro Ser Leu Phe Leu Phe Thr  
 50 55 60

Ile Asn Ser Ser Ser Leu Ser Gly Gly Ser Val Thr Arg Cys Ala Ala  
 65 70 75 80

Gly Lys Ile Pro Leu Asp Thr Phe Ala Ala Val Cys Leu Phe Ile Thr  
 85 90 95

Leu Leu Gly Leu Ile Leu Pro Pro Ala Gly Thr Val Cys Val Ala Ala  
 100 105 110

Arg Glu Trp Gly Ser Ala Cys Arg Thr Ser Arg Glu His Gly Glu Pro  
 115 120 125

Leu Ala Thr Tyr Gly Ser Leu Pro Leu Ser Glu Ala Glu Ser Asn Glu  
 130 135 140

Gln Arg Ser Arg Ile Pro Arg Thr His Cys Arg Ala His Leu Leu Leu  
 145 150 155 160

Ser Ala Ala Ser Ser Arg Gly Lys Arg Phe Leu Gly Ala Val Ala His  
 165 170 175

Ala Leu Glu Cys Phe Ser Trp Gln Lys Asn Val Pro Ala Ile Trp Thr  
 180 185 190

Thr Lys Ala Pro Gly Gly Thr Cys Ser Ala Leu Asn Gly Ile Arg Val  
 195 200 205

Leu Ser Leu Leu Trp Ile Ile Ser Gly His Thr Ser Gln Met Thr Ala  
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Trp Leu Ser Leu Gly Trp Lys Asp Gly Gly His Glu Arg Pro Leu Val  
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Met Ser Gly Pro Ser Val Gly Ile Gly Asp Thr Arg Glu Ala Thr Ser  
 245 250 255

Gly Trp Leu Ser Ala Ser Ser Phe Leu Lys Met His Gln Asn Ser Asp  
 260 265 270

Lys Gly Ile Thr Pro Lys Gly Ile Leu Arg Tyr Phe Leu Ser His Leu  
 275 280 285

Val Arg Leu Gln Pro Leu His Leu Tyr Ser Met Cys Leu Leu Val Gly  
 290 295 300

Leu Phe Ser Leu Val Pro Trp Gly Pro Val Trp Glu Met Pro Lys Phe  
 305 310 315 320

His Trp Asp Asn Cys Arg Gln Ala Trp Trp Thr Asn Leu Leu Leu Leu  
 325 330 335

Asn Asn Phe Val Ser Val Lys Asn Ala Cys Asn Gly Trp Thr Trp Tyr  
 340 345 350

Leu Ala Asn Asp Phe Gln Phe His Leu Thr Thr Pro Val Ile Ile Phe  
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Ile His Val Lys Ser Thr Gln Ile Leu Ile Leu Leu Gly Ala Met Leu  
 370 375 380

Phe Leu Ala Ser Phe Thr Ala Thr Ala Leu Ile Thr Leu Ala Tyr Lys  
 385 390 395 400

Leu Pro Val Val Ala Pro Ser Glu Thr Arg Thr Ser Arg Gly Gly Leu  
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Leu Asn Ala Arg Leu Phe Thr Leu Cys Pro Leu Val His Gly Lys Ser  
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Gly Tyr Glu Thr Phe Gly Leu Asp Gly Lys Ala Asp Cys Leu Leu Ala  
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Ser Lys Leu Leu Asn Leu Ser Thr Cys Thr Gly Asn Glu Gln Val Cys  
 450 455 460

Pro Lys Cys Thr Phe Gly Leu Ala Asp Tyr Ser Asn Gly His Leu Arg  
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Asp Leu Asp Ser Leu Cys His Val Gln Ile Lys His Asn Ile Leu Ala  
 485 490 495

Tyr Phe Leu Val Phe Phe Ser Glu Glu Ala Ile Val Leu Tyr Phe Val  
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Glu Tyr Tyr Thr Lys Pro Tyr Cys Arg Phe Gly Pro Val Leu Val Gly  
 515 520 525

Leu Phe Leu Ser Ile Tyr Met His Gln Asn His Gln Glu Asn Ile Leu  
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Arg Thr Lys Leu Gln Leu Ser Thr Lys Pro Ser Thr Gly Pro Cys Gly  
 545 550 555 560

Arg Arg Leu Trp Ala Glu Ser Ser Leu Arg Ala Thr Glu Asp Met Glu  
 565 570 575

Val Trp Lys Arg Leu Gln Ala Leu Leu Ser Gly Ser His Pro Val Pro  
580 585 590

Leu Lys Val Thr Asn Arg Thr His Arg Arg Ala Lys Gln Ile Lys Gly  
595 600 605

Phe Asn Gly Lys Glu Ser Ser Pro Gly Leu Val Asn Arg Val Leu Ser  
610 615 620

Trp Asp Ile Trp Ser Phe Leu Ser Ser Ile Ser Tyr Ala Arg Tyr Leu  
625 630 635 640

Val His Pro Ile Leu Ile Ile Leu Tyr Asn Gly Leu Gln Glu Thr Leu  
645 650 655

Ile His His Thr Asp Thr Asn Met Phe Tyr Leu Phe Ser Gly His Arg  
660 665 670

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Pro Cys Gln Glu Leu Lys Gln His Leu Leu Gly His Glu Cys Ser Gly  
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